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March 30, 2004, 18:11:59; Search time 5268 Seconds (without alignments) 11082.587 Million cell updates/sec
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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larity 100.0%; Pred. No. 1.4e-261;
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Immunization of dairy cattle with chim
Streptococcus infection
Patent: WO 0196379-A 21 20-DEC-2001;
The University of Saskatchewan (CA)
Location/Qualifiers
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Perez-Casal, J.F., Bolton, A., Song, X.-M., Willson, P. and Potter, A.A. Use of the surface proteins GapC and Mig of Streptococcus dysgalactiae as protective antigens against mastitis in Unpublished
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Perez-Casal, J.F., Bolton, A., Song, X.-M., Willson, P. and Potter, A.A. Direct Submission
Submitted (02-MAY-2001) VIDO, University of Saskatchewan, 120
Veterinary Rd, Saskatoon, SK S7N 5E3, Canada
Location/Qualifiers
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Pred. No. 1.1e-154;
); Mismatches 21;
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DEFINITION Sequence 11 from patent US 6660270.

ACCESSION AR437347
VERSION AR437347.1 GI:40202278

KEYWORDS
SOURCE
Unknown.
Unclassified.
Unclassified.

TITLE Immunization of dairy cattle with chimeric GapC protein against streptococcus infection
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RESULT

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                                                    Score 815.8; DB 6;
Pred. No. 2.3e-154;
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Patent: US 6660270-A 11 09-DEC-2003
Location/Qualifiers
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829; Conservative
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|mol_type="unassigned DNA"
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Patent: WO 0196379-A 11 20-DEC-2001;
The University of Saskatchewan (CA)
Location/Qualifiers
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Pred. No. 2.3e-154;
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Streptococcus.
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Bolton, A.J., Perez-Casal, J., Fontaine, M. and Potter, A./
Immunization of dairy cattle with gapc protein against
Streptococcus infection
Streptococcus infection
Patent: WO 0196381-A 3 20-DEC-2001;
The University of Saskatchewan (CA)
Location/Qualifiers
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Pred. No. 2.3e-154;
); Mismatches 22;
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Streptococcus dysgalactiae
Bacteria, Firmicutes, Lactobacillales,
Streptococcus.
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Matches 829; Conservative
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LKYDTTOGREDGTVEVKEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEATGFFAK
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PIVSSDIVGVSYGSLFDATQTKVMEVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKI
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(NAPlr)

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Fujino, M., Yamakami, K. and Yoshizawa, ...
Fujino, M., Yamakami, K. and Yoshizawa, ...
Direct Submission
Submitted (15-JUL-2002) Nobuyuki Yoshizawa, national defense medical colllege, department of public health; 3-2 namiki, tokorozawa, saitama 359-8513, Japan (E-mail:yosizawa@cc.ndmc.ac.jp, tokorozawa, saitama 359-8513, Japan (E-mail:yosizawa@cc.ndmc.ac.jp, Tel:81-42-995-1575, Fax:81-42-996-5196)
Location/Qualifiers
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/EC_number="1.2.1.12"
/function="glyceraldehyde-3-phosphate dehydrogenase;
plasmin binding activity"
/note="glyceraldehyde-3-phosphate dehydrogenase (GAP)
plasmin binding protein; nephritogenic antigen"
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/evidence=experimental
/transl_table=11
/product="nephritis-associated plasmin receptor"
/protein_id="BAC05496.1"
/db_xref="G1:21886630"
acute poststreptococcal glomerulonephritis (APSGN)
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mol_type="genomic DNA"
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Fujino, M., Yamakami, K. and Yoshizawa, N.
Direct Submission
Submitted (15-JUL-2002) Nobuyuki Yoshizawa, national defense medical colllege, department of public health; 3-2 namiki, tokorozawa, saitama 359-8513, Japan (E-mail:yosizawa@cc.ndmc Tel:81-42-995-1575, Fax:81-42-996-5196)
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                   TTATGACTACAATCCACGCTTACACTGGTGACCAAATGATCCTTGACGGACCAC
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae
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Further studies of nephritis-associated plamin receptor
acute poststreptococcal glomerulonephritis (APSGN)
Unpublished
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mol_type="genomic DNA"

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db_xref="taxon:1314"
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plasmin binding activity"
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plasmin binding protein; nephritogenic antigen"
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Pred. No. 1.4e-147;
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AKALHDAFGIQKGLMTTIHAYTGDQMILDGPHRGGDLRRARAGAANIVPNSTGAAKAI
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PIVSSDIVGVSYGSLFDATQTKVMEVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKI
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Fujino, M., Yamakami, K. and Yoshizawa, N.
Direct Submission
Submitted (15-JUL-2002) Nobuyuki Yoshizawa, national defenedical colllege, department of public health; 3-2 namix. tokorozawa, saitama 359-8513, Japan (E-mail:yosizawa@cc.? Tel:81-42-995-1575, Fax:81-42-996-5196)
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/gene="naplr"
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/function="glyceraldehyde-3-phosphate dehydroge:
plasmin binding activity"
/note="glyceraldehyde-3-phosphate dehydrogenase
plasmin binding protein; nephritogenic antigen"
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For nephritis-associat
Type 12.
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Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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/db_xref="GI:21886626"
   CAACTCAAACTAAAGTAATGGAAGTTGACGGATCACAATTGGTTAAAGTTGTAT
                             ATGACAATGAATGTCTTACACTGCTCAACTTGTTCGTACACTTGAGTATTTC
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Further studies of nephritis-associated plamin receptor
acute poststreptococcal glomerulonephritis (APSGN)
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/strain="T Type 12"
/db_xref="taxon:1314"
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Pred. No. 1.3e-147;
0; Mismatches 43;
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evidence=experimental
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AB088215
Streptococcus pyogenes naplr gene for nephritis-associated plasmin receptor, complete cds, strain: T Type 1.
AB088215
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Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales;
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KEAAEKHLHANGAKKVVITAPGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPM
AKALHDAFGIQKGLMTTIHAYTGDQMILDGPHRGGDLRRARAGAANIVPNSTGAAKAI
GLVIPELNGKLDGAAQRVPVPTGSVTELVVTLDKNVSVDEINAAMKAASNDSFGYTED
PIVSSDIVGVSYGSLFDATQTKVMEVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKI
                                                                                                                                                                                                                                                                                                                                                                          trans| table=11
|product="nephritis-associated plasmin receptor"
|protein_id="BAC05495.1"
|db_xref="GI:21886628"
|translation="MVVKVGINGFGRIGRLAFRRIQNIEGVEVTRINDLTDPNMLAHL
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                                                        Chases 1 to 1104)
Fujino, M., Yamakami, K. and Yoshizawa, N.
Direct Submission
Submitted (15-JUL-2002) Nobuyuki Yoshizawa, national defe medical colllege, department of public health; 3-2 namiki tokorozawa, saitama 359-8513, Japan (E-mail:yosizawa@cc.n Tel:81-42-995-1575, Fax:81-42-996-5196)
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                                                                                                                                                                                                                                                                          /gene="naplr"
/EC_number="1.2.1.12"
/function="glyceraldehyde-3-phosphate dehydrogen
plasmin binding activity"
/note="glyceraldehyde-3-phosphate dehydrogenase
plasmin binding protein; nephritogenic antigen"
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Yoshizawa, N., Yamakami, K. and Fujino, M.
Further studies of nephritis-associated plamin receptor
acute poststreptococcal glomerulonephritis (APSGN)
Unpublished
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                                                                                                                                                                        /organism="Streptococcus pyogenes/mol_type="genomic DNA"/strain="T Type 1"/db_xref="taxon:1314"
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Pred. No. 2.9e-147;
); Mismatches 44;
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evidence=experimental
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CTGCTAAAGCTATCGGTCTTGTTATCCCAGAACTTAACGGTAAACTTGACGGTGCTGCTGCACAC
                                                                                                                                                                      TTTCTGTTGACGAAATCAACGCTGCTATGAAAGCTGCTTCAAACGACAGTTTCGGTTACA
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Boyle, M.D.P., Lottenberg, R., Broder, C. and Von Mering, G
Bacterial plasmin receptors as fibrinolytic agents
Patent: US 6136323-A 1 24-OCT-2000;
Location/Qualifiers
1. .1125
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Pred. No. 2.9e-147;
); Mismatches 44;
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Sequence 1 from patent US 6136323.
AR135510
AR135510.1 GI:14476182
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/codon_start=1
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/evidence=experimental
/transl_table=11
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PIVSSDIVGVSYGSLFDATQTKVMEVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKI
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48. .53
/gene="plr"
73. .78
/gene="plr"
/note="putative"
99. .105
/gene="plr"
115. .1125
/gene="plr"
/function="plasmin binding protein"
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Pred. No. 2.9e-147;
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                                                                CAAACTGTTTAGCTCCTATGGCTAAAGCTCTTCACGATGCATTTGGTATCCAAA
                                                                                                                                                                     GTGGTGACCTTCGTGCTGCTGCTGGTGCTGCAAACATTGTTCCTAACTCAA
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Streptococcus pyogenes plasmin receptor (plr) gene, cor M95569.

M95569.1 GI:153762
plasmin binding protein; plasmin receptor.
Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales; Streptococcace: Streptococcus.

1 (bases 1 to 1156)
Lottenberg, R., Broder, C.C., Boyle, M.D., Kain, S.J., Scland Curtiss, R. III.
Cloning, sequence analysis, and expression in Escheric streptococcal plasmin receptor
J. Bacteriol. 174 (16), 5204-5210 (1992)
92355491
1322883
Original source text: Streptococcus pyogenes DNA.
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Location/Qualifiers
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PIVSSDIVGVSYGSLFDATQTKVMEVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKI
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ptor
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Yoshizawa, N., Yamakami, K. and Fujino, M.
Nephritis-associated plasmin receptor (naplr) of group A
Streptococci pyogenes T type 4
Unpublished
2 (bases 1 to 2326)
Yoshizawa, N., Yamakami, K. and Fujino, M.
Direct Submission
Submitted (07-JUN-2002) Public Health, National Defense Medical
College, 3-2, Namiki, Tokorozawa, Saitama 359-8513, Japan
Location/Qualifiers
CTGAAGATCCAATTGTTTCTTCAGATATCGTAGGCGTGTCATACGGTTCATTGTTTGACG
                  CTGAAGATCCAATCGTTTCTTCAGATATCGTAGGCGTATCATACGGTTCATTGTTTGACG
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Streptococcus pyogenes nephritis-associated plasmin recept (naplr) gene, complete cds.
AF520813
AF520813.1 GI:21686541
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Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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885. .1895
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M1 GAS strain SF370, section 23 of 167 of
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Score 780.6; DB 1;
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the complete genome.
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AE006494.1 GI:13621549
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gene="bacA"
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Submitted (10-APR-2001) Department of Microbiology and Immunology, University of Oklahoma Health Sciences Center, 940 SL Young Blvd, Oklahoma City, OK 73104, USA

Location/Qualifiers
                                                                                                                                                                          , Lyon, K., ., Lin, S.,
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Ferretti, J.J., McShan, W.M., Adjic, D., Savic, D., Savic, G. Primeaux, C., Sezate, S.S., Surorov, A.N., Kenton, S., Lai, H.Qian, Y., Jia, H.G., Najar, F.Z., Ren, Q., Zhu, H., Song, L., Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E. Complete genome sequence of an M1 strain of Streptococcu Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
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protein glnQ - Archaeoglobus fulgidus
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transporter, ATP-binding protein (glnQ) [Archae
                                                                         Streptococcaceae
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protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Streptococcus pyogenes Ml/mol_type="genomic DNA"
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Streptococcus pyogenes M1 GAS
Streptococcus pyogenes M1 GAS
Bacteria, Firmicutes, Lactobacillales,
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   SOURCE
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EAMLFDEPTSALDPEMVGEVLKTMQDLAKSGLTMIIVTHEMEFARDVSDRIIFMDKGL
ITEEGSPQQIFENPTQDRTKEFLQRFLK"
complement (2432. .4000)
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                                                                                                                                                                                                                                                                                                                                                                                                 - Synechocystis sp. (strain PCC 6803)
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(AF169967) BacA [Flavobacterium johnsoniae]"
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CAAACTGTTTAGCTCCTATGGCTAAAGCTCTTCACGATGCATTTGGTATCCAAAAAGGTC
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AE014140 AE014074
AE014140.1 GI:21903894
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9206. .9976

/gene="SPy0285"

/note="Best Blastp hit = sp|P80866|V296 BACSU VEGE'

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/note="SPy0285"

/note="SPy0296"

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/note="SPy0296"

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/note="Sporter (ATP-binding protein) [Bacillus sulland s
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Pred. No. 2.6e-147;
0; Mismatches 44;
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7915. .9084
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/note="synonym: SPy07147. .7908
/gene="mecA"
/note="Best Blastp h
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/transl_table=11
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/gene="rgpG"
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Submitted (14-JUN-2002) Laboratory of Human-Bacterial Pathogenesis,
Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St.,
Hamilton, MT 59840, USA
Location/Qualifiers
1. .50029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes MGAS315
Streptococcus pyogenes MGAS315
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.

1 (bases 1 to 50029)
Beres, S.B., Sylva, G.L., Barbian, K.D., Lei, B., Hoff, J.S.,
Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F.,
Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M. and
Musser, J.M.
Genome sequence of a serotype M3 strain of group A Streptococcus:
Phage-encoded toxins, the high-virulence phenotype, and clone
BCT 19-JUL-;
the complete
                                                        TTATGACTACAATCCACGCTTATACTGGTGACCAAATGATCCTTGACGGACCACACGTG
                                                                                                                                                                                                                                                                                                                                                                                 TTTCTGTTGACGAAATCAACGCTGCTATGAAAGCTGCTTCAAACGACAGTTTCGGTTACA
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2 (bases 1 to 50029)
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LSGYTPYSRQEAGPDVALIEALCKAGIAVIAEGKIHSPEEAKKINDLGVAGIVVGGAI
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M1 GAS]"
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M1 GAS]"
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Pred. No. 2.4e-147;
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Search completed: March 31, 2004, 00:58:07 Job time : 5274 secs

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- 2004 Compugen Ltd
GenCore
(c) 1993
           Copyright
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nucleic search, using sw model OM nucleic

Search time 566 Seconds (without alignments) March 30, 2004, 18:05:29 Run on:

dates/sec

1347

...ttgcaaaaatcgctaaataa

US-10-650-369-21 1347 Title: Perfect

atgaaaaaaataacagggat score: Sequence:

Gapext IIY NUC IDENTITY Gapop 10. Scoring table:

1.0

residues 3373863 segs, 2124099041 Searched: hits satisfying chosen parameters: o F Total number

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Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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PolyGap4; GapC; plasmin binding protein; epitope; infection; vaccine; immunisation; mastitis; therapy; gene; ds.
                                            Streptococcus GapC multiepitope fusion PolyGap4 DNA.
          ABA91327 standard; DNA; 1347 BP
                              (revised)
(first entry)
                              29-AUG-2003
08-APR-2002
                    ABA91327;
RESULT 1
ABA91327
```

Streptococcus dysgalactiae. Streptococcus agalactiae. Streptococcus parauberis. Chimeric. WO200196379-A2

11-JUN-2001; 2001WO-CA000836. 20-DEC-2001.

2000US-0211247P.

12-JUN-2000;

Fontaine M; (UYSA-) UNIV SASKATCHEWAN. Perez-Casal J, Potter AA,

WPI; 2002-098051/13. P-PSDB; AAM50664.

ς. Ω Novel GapC multiple epitope fusion polypeptide comprising antigenic determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, parauberis, or S. iniae GapC protein useful for treating mastitis in vertebrates.

Example 4; Fig 6A-C; 116pp; English.

The present sequence is that of a chimeric gene encoding a multiple epitope fusion protein (see AAM50664), designated PolyGap4, comprising the entire amino acid sequence of the Streptococcus dysgalactiae GapC plasmin binding protein in addition to unique amino acid sequences from the Streptococcus agalactiae GapC proteins.

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Fontaine M;
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P-PSDB; AAM50665.
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The gapC gene sequences used to construct the chimeric gene were prepared by PCR amplification of selected polynucleotide sequences from the genomic gapC genes using the primers given in ABA91335-42. After assembly, the chimeric gene was inserted into plasmid pAA555. PolyGal4 is an example of novel GapC multiple epitope fusion proteins of the invention that comprise epitopes from 1 or more of S. dysgalactiae, S. garauberis, Streptococcus uberis and Streptococcus iniae (see AAMS0665-69). The multiple epitope fusion proteins are produced using claimed host-vector systems and used in claimed vaccines for treating or preventing a bacterial infection in a vertebrate, especially a streptococcal infection, and particularly mastitis. They are also used in claimed methods of detecting Streptococcus antibodies. The multiple epitope protein is capable of eliciting broad immunity against a variety of streptococcal infections while minimising the number of antigens present in the final formulation and concomitantly reducing production costs. (Updated on 29-AUG-2003 to standardise OS field)
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                                                              DysGapC; GapC; plasmin binding protein; epitope; infection; vaccine; immunisation; mastitis; therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                 Streptococcus dysgalactiae gapC plasmin binding protein gene
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S
                                                                      is in
Novel GapC multiple epitope fusion polypeptide comprising antigenic determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, parauberis, or S. inlae GapC protein useful for treating mastitis in
                                                                                                                                                                    3; Fig 1A-B; 116pp; English
                                                                                                   vertebrates
                                                                                                                                                                  Example
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The present sequence is that of the coding region of the gene encoding the GapC plasmin binding protein, DysGapC (see AAM50665), of the GapC plasmin binding protein, DysGapC (see AAM50665), of streptococcus dysgalactiae ATCC 43078, an isolate from a case of bovine mastitis. The gene was obtained by PCR amplification of chromosomal DNA using the primers given in ABA9133-34. The invention relates to novel GapC multiple epitope fusion proteins that comprise epitopes from 1 or more of Streptococcus dysgalactiae, Streptococcus agalactiae, Streptococcus agalactiae, Streptococcus iniae (see AAM50665-69). A claimed example is PolyGap4 (see AAM50664). The multiple epitope fusion proteins are produced using claimed host-vector systems and used in claimed vaccines for treating or preventing a bacterial infection in a vertebrate, especially a streptococcal infection in a vertebrate, especially a streptococcal infections while minimising the number of antigens present in the final formulation and concomitantly reducing production costs

1096 1156 ö 760 700 556 616 280 736 400 460 856 580 976 640 676 340 796 916 GTTACA TTGACGGAACTGTTGAAGTTAAAGAAGGTGGATTTGAAGTAAACGGAAACTTCATCAAAG CTGCAC TAACG TTTCA ACCGTG ACCGIG CTGGTG TGCAC TCGTTC CTAACG STACTA Gaps gaaggregatregaggraacggreaarreg GTGCTAAAAAGTTGTTATCACAGCTCCTGGTGGAAACGACGTTAAAACAGTTG' ACACTAACCACGACATTCTTGACGGTACTGAAACAGTTATCTCAGGTGCTTCAT titcigitgacgaaatcaacgctgctatgaaagctgcttcaaacgacagtttcg TITCIGCIGAACGCGAACCAGCAACAITGACIGGGCIACIGAIGGCGIAGAAA Grectalala a de la contraca de contraca de contra de la contra de la contraca del contraca de la contraca de la contraca de la contraca del contraca de la contraca del contraca del contraca de la contraca de la contraca de la contraca del cont CTGCTAAAGCTATCGGTCTTGTTATCCCAGAATTGAATGGTAAACTTGATGGTG 0 Length 1011 0 Other; Indels GTGGTGACCTTCGTCGTGCTCGTGCTGCTGCTGCAAACATTGTTC T; 0 U; Score 815.8; DB 6; Pred. No. 3.4e-207;); Mismatches 22; G; 300 C; 216 TCGATGGTACTGTTGAAGTTAAA .. 0 1011 BP; 295 A; 200 Query Match Best Local Similarity 97.4%; Matches 829; Conservative 161 557 701 Sequence 497 617 857 1037 221 341 797 581 641 281 677 401 461 521 917 977 1097 A D Бр dd d d 5 C a g ઠે à ò à à $\stackrel{>}{\circ}$ ठे ö 슝

1276 1000 940 880 TITCTGTTGACGAAATCAACGCTGCTATGAAAGCTGCTTCAAACGACAGTTTCGGTTACA CTGAAGATCCAATTGTTTCTTCAGATATCGTAGGCGTGTCATACGGTTCATTGTTTGACG CAACTCAAACTAAAGTTATGGAAGTTGACGGATCACAATTGGTTAAAGTTGTATCATGGT CAACTCAAACTAAAGTTATGGAAGTTGACGGATCACAATTGGTTAAAGTTGTATCATGGT ATGACAATGAAATGTCTTACACTGCTCAACTTGTTCGTACACTTGAGTATTTTGCAAAAA TCGCTAAATAA 1347 101 TCGCTAAATAA 1001 941 1277 761 1157 821 881 1337 엄 Q 8 ö අ δ ਨੇ ਨੇ

RESULT 3 ABA91248

ABA91248 standard; DNA; 1011

ABA91248;

entry) (first

Streptococcus dysgalactiae gapC gene

GapC; plasmin-binding protein; infection; mastitis; vaccine; diagnosis; gene therapy; gene; ds.

Streptococcus dysgalactiae.

WO200196381-A2

20-DEC-2001.

11-JUN-2001; 2001WO-CA000838

12-JUN-2000; 2000US-0211022P

(UYSA-) UNIV SASKATCHEWAN

Potter AA; Fontaine M, Perez-Casal Bolton AJ,

WPI; 2002-130725/17. P-PSDB; AAM50639.

Novel isolated GapC protein of Streptococcus dysgalactiae, S.agalactiae, S.uberis, S.parauberis, or S.iniae, useful as vaccine component for treating streptococcal infection which causes mastitis in vertebrates.

1; Fig 1A-B; 107pp; English Example

The present sequence is that of the coding region of the GapC plasmin binding protein gene of Streptococcus dysgalactiae ATCC 43078, a clinical isolate from a case of bovine mastitis. The gene was amplified from chromosomal DNA by PCR using the primers given in ABA91253 and ABA91254. The pcr product was cloned into expression vector pET15N, creating capable of eliciting an immune response in a vertebrate. The invention provides the GapC plasmin binding proteins of 5 treptococcus species, as well as recombinant vectors, host cells and vaccine compositions comprising GapC polynucleotides or proteins. The streptococcal infection, and mastitis in particular (claimed). A streptococcal infection, and mastitis in sused in a claimed method of treating or preventing a bacterial infection, such as a streptococcal infection, infection, such as a streptococcal infection.

Other; 0 0 0; G; 300 216 ΰ A; 200 Sequence 1011 BP; 295

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 3; DB 6;
3.4e-207;
nes 22;
 Score 815.8;
Pred. No. 3.4e
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Conservative
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Best Local Similarity
Matches 829; Conser
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid containing the vector; (3) an isolated on polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated oplypeptide, (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influence the activity of identifying a compound that influence the biological pathway in which a proliferation or that has an activity against a biological pathway in which a proliferation required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a civity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for relating proteins or severable for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for retional drug discovery programs, or for screening homologous nucleic acids required for proliferation to isolate candidate molecules for retional drug discovery programs, or for screening homologous nucleic acids required for proliferation to isolate candidate molecules for retional companies. Note: The sequence is one of the target of companies of the printed specification, but was obtained in clear sequences. The sequence is one of the target of the printed specification, but was obtained in the printed port sequences.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screfor homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Pred. No. 8.5e-198;
0; Mismatches 44;
                                    cell
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Yamamoto R,
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                  s; prokaryotic essential
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GJ,
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2001US-00948993.
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2002US-00072851.
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Best Local Similarity 94.8%;
Matches 807; Conservative
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                                                                                          Streptococcus pyogenes
Prokaryotic essential
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B; ABU46455.
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                                     ds;
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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TTGATGGAACAGTTGAAGTTAAAGGTGGATTTTGAAGTAAACGGAAACTTCA
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This sequence encodes the S. pyogenes plasmin receptor. This sequence was isolated from the S. pyogenes clinical isolate 64/14. The plasmin receptor has a very high affinity for plasmin which, when bound, retains its enzymatic activity but is not regulated (inhibited) by alpha-2-antiplasmin. The receptor protein, when administered concurrently or sequentially, prolongs the activity of plasminogen activator (PA) so allows a reduction in dose, and thus lowers the risk of bleeding, and may prevent reocclusion of blood vessels. The protein may be coupled to a fibrin-specific monoclonal antibody to provide targetting to clots. The plasmin receptor may be useful in human or veterinary medicine, for treatment of thrombosis and pulmonary embolism, and for solubilising clots in catheters or shunts. (Updated on 25-MAR-2003 to correct PF
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Pred. No. 8.9e-198;
0; Mismatches 44;
                                                                                                "Plasmin receptor"
                               Location/Qualifiers
115. .1125
/*tag= a
/product= "Plasmin re
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illarity 94.8%;
Conservative (
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90US-00524411
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Streptococcus pyogenes.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    Von Mering G,
                                                                                                                                                                                                                                                                 29-MAR-1989;
16-MAY-1990;
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Plasmin receptor; isolate 64/14; plasmin; alpha-2-antiplasmin; plasminogen activator; bleeding; reocclusion; thrombosis; pulmonary embolism; clots; ss.

Plasmin receptor DNA.

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                                                                                            AACGIGITCCIGITCCAACTGGATCAGTAACTGAGTTGGTTGTAACTCTTGATA
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Streptococcal infection; antihelminthic; ds.
Boyle MDP;
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90US-00524411.
92US-00928462.
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16-MAY-1990;
10-AUG-1992;
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                                                                                                                        Polynucleotide sequence AAC66140 encodes the Streptococcal plasmin receptor protein AAY85681. The protein is used in a method for raising immune response in a mammal. The method comprises administering the plasmin receptor protein. The method is useful as a vaccination against group A Streptococcal infections and potentially against a broad range infections associated with pathogens expressing glyceraldehyde-3-phosphate dehydrogenase (GAPDH) or GAPDH-like proteins at their cell surfaces. The vaccine has antibacterial and antihelminthic activity
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                            Raising an immune response in a mammal, especially for vaccination against group A streptococcal infections, comprises administering a isolated streptococcal plasmin receptor protein.
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                                                                                                                                                                                                                                                                                                              Length 1125;
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Pred. No. 8.9e-198;
0; Mismatches 44;
                                                                                              Disclosure; Col 25-28; 17pp; English
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ilarity 94.8%;
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P-PSDB; AAY85681
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. (I) are used to detect Streptococcus in a bological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying streptococcus proteins
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CAACTCAAACTAAAGTAATGGAAGTTGACGGATCACAATTGGTTAAAGTTGTAT
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                                                                                                                                                                                                                                                                                                                   Streptococcus; GAS; GBS; group B streptococcus; Streptococcus aggroup A streptococcus; Streptococcus; group A streptococcus; Streptococcus pyogenes; antibacterial; gantiinflammatory; infection; vaccine; meningitis; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of disease caused by Streptococcus bacteria, such as meningitis, detecting a compound that binds to the protein.
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2000GB-00028727.
2001GB-00005640.
                                                                                                                                                                                                standard; DNA; 1008
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-PSDB; ABP29960.
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INST GENOM:
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24-NOV-2000;
07-MAR-2001;
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Tettelin H;
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Length 1008;

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Query Match

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                                                                                             TTATGACTACAATCCACGCTTATACTGGTGACCAAATGATCCTTGACGGACCACACGTG
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          Gaps
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    97;
  5.4e-197
 Pred. No. 5.46
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The present sequence is that of the coding region of the gene encoding the GapC plasmin binding protein, AgalGapC (see AAM50666), of Streptococcus agalactiae ATCC 27541. The gene was obtained by PCR amplification of chromosomal DNA using the primers given in ABA9133-34.

The invention relates to novel GapC multiple epitope fusion proteins that comprise epitopes from 1 or more of Streptococcus dysgalactiae, Streptococcus agalactiae, Streptococcus dysgalactiae, Streptococcus iniae (see AAM50665-69). A claimed example is PolyGap4 (see AAM50664). The multiple epitope fusion proteins are produced using claimed host-vector systems and used in claimed vaccines for treating or preventing a bacterial infection in a vertebrate, especially a streptococcal infection and particularly mastitis. They are also used in claimed methods of detecting Streptococcus antibodies. The multiple epitope proteins are capable of eliciting broad immunity against a variety of streptococcal infections while minimising the number of antigens present in the final formulation and concomitantly reducing production costs
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S. uberis,
                    Novel GapC multiple epitope fusion polypeptide comprising antige
determinant of Streptococcus dysgalactiae, S. agalactiae, S. ube
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The present sequence is that of the coding region of the GapC plasmin binding protein gene of Streptococcus agalactiae ATCC 27541. The gene was amplified from chromosomal DNA by PCR using the primers given in ABA91253 plasmid pMF521c. The gene encodes a GapC plasmin binding protein (see plasmid pMF521c. The gene encodes a GapC plasmin binding protein (see AAM50640) that is capable of eliciting an immune response in a creeptococcus species, as well as recombinant vectors, host cells and vaccines compositions comprising GapC polynucleotides or proteins. The vaccines are used to treat or prevent a bacterial infection, especially a streptococcal infection, and mastitis in particular (claimed). A streptococcal infection, and mastitis in sused in a claimed method of treating or preventing a bacterial infection, such as a streptococcal infection, especially mastitis. S. agalactiae is a common pathogen associated with mastitis in cattle, horse, sheep and goat. It also causes septicemia, meningitis, bacteraemia, impetigo, arthritis, urinary tract infections, abcesses, spontaneous abortion, etc
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Sequence 1011 BP; 305 A; 204 C; 213 G; 289 T; 0 U; 0 other; Query Match S2.1%; Score 702.2; DB 6; Length 1011; Best Local Similarity B9.1%; Pred. No. 7e-177; Pred. D. 7e-177; Pred. S. 758; Conservative O; Mismatches 93; Indels O; Gaps G	737 ACACTAACCACGACATTCTTGACGGTACTGAAACAGTTATCTCAGGTGCTTCATGTACTA 79 401 ACACTAACCACGATATCCTTGATGGAACTGAAACAGTTATCTCAGGTGCTTCATGTACTA 46 797 CAAACTGTTTAGCTCCTATGGCTAAAGCTCTTCACGATGCATTTGGTATCCAAAAAGGTC 85	461 CAAACTGTCTTGCTCCAATGGCTATACAAGACAACTTTGGTGTGTGT		Oy 1037 AACGTGTTCCAACTGGATCAGTAACTGAGTTGGTTGTAAAAACG 1096	1157 CTGAAGATCCAATTGTTTCTTCAGATATCGTAGGCGTGTCATACGGT	881 CTACTCAAACTAAAGTTCAAACTGTTGACGGTAACCAATTGGTTAAAGTTGTTTCA 1277 ATGACAATGACTTACACTGCTCAACTTGTTCGTACACTTGAGTATTTTGCA 941 ACGATAACGAAATGTCATACACTTCACAACTTGTTCGTACACTTGAGTACTTTGCA	1337 TCGCTAAATAA 1347 	SULT 11 N71527_17/c

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RESULT 11
ABN71527_17/c
Continuation (18 of 22) of ABN71527 from base 1700001 (Streptococcus polynucleotide SEQ
WP Sequence split into 22 fragments LOCUS ABN71527 Accession Abn71527
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1157 CTGAAGATCCAATTGTTTCTTCAGATATCGTAGGCGTGTCATACGGTTCATTGTTTGACG 1216

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Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be caid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
CTGAAGATCCAATCGTATCATCTGATATCGTTGGTATTTCATACGGTTCATTGTTTGATG 29883
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                                                                                                                                                                                                                                                                                                                            Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agroup A streptococcus; Streptococcus pyogenes; antibacterial; grantinflammatory; infection; vaccine; meningitis; gene therapy;
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2000GB-00028727.
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P-PSDB; ABP30758.
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24-NOV-2000;
07-MAR-2001;
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                       Gaps
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 Length 1008;
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95; Indels
Query Match
Best Local Similarity 88.8%; Pred. No. 3.2e-175
Matches 753; Conservative 0; Mismatches 95
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| TTGCTAAATAA 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aucheus, Salmonella typhi, Klebsiella pneumoniae, seudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can also useful to screen for homologous nucleic acids equence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed pot fermines.
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                                                             cellular proliferation gene; antibiotic;
                                    cellular proliferation protein
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Pred. No. 9.6e-172; ); Mismatches 95;
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                                    Streptococcus pneumoniae DNA for
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2000US-0206848P.
2000US-0207727P.
2000US-0242578P.
2000US-0253625P.
2000US-0257931P.
2001US-0269308P.
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drug design
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Xu HH;
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P-PSDB; AAU37999.
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Best Local Similarity
Matches 753; Conser
                                                           Antisense; ds;
antibacterial;
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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             13-FEB-2002
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immunisation; mastitis; therapy; gene; ds.
.037 AACGTGTTCCAACTGGATCAGTAACTGAGTTGGTTGTAACTGTTAAAACG
                                                                                                                                                                                                                                                                     CAACTCAAACTAAAGTTATGGAAGTTGACGGATCACAATTGGTTAAAGTTGTATCATGGT
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                                                                                                                                                                                                                                                                                                                                                                                              preventing a bacterial infection in a vertebrate, especially a streptococcal infection, and particularly mastitis. They are also used in claimed methods of detecting Streptococcus antibodies. The multiple epitope proteins are capable of eliciting broad immunity against a variety of streptococcal infections while minimising the number of antigens present in the final formulation and concomitantly reducing
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                                                                                                                Novel GapC multiple epitope fusion polypeptide comprising antigenic determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, parauberis, or S. iniae GapC protein useful for treating mastitis in vertebrates.
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Pred. No. 1.8e-170;
0; Mismatches 108;
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                                 Fontaine
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Best Local Similarity 87.3%;
Matches 743; Conservative
                              Perez-Casal J,
(UYSA-) UNIV SASKATCHEWAN
                                                              2002-098051/13
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P-PSDB; ABA50669
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production costs
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                            Potter AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated GapC protein of Streptococcus dysgalactiae, S.agalactiae, S.uberis, S.parauberis, or S.iniae, useful as vaccine component for treating streptococcal infection which causes mastitis in vertebrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GapC; plasmin-binding protein; infection; mastitis; vaccine; diagnosis
gene therapy; gene; ds.
CTTCAGTAGAAGAAATCAATGCAGCTATGAAAGCAGCAGCTAACGATTCATACGGTTACA
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Best Local Similarity 87.3%; Pred. No. 1.8e-170;
Matches 743; Conservative 0; Mismatches 108;
polynucleotide encoding a GapC protein is used treating or preventing a bacterial infection, sinfection, especially mastitis
                                 Sequence 1011 BP; 305 A; 191 C; 213 G; 302
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Search completed: March 30, 2004, 23:30:05 Job time : 574 secs

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SUMMARIES	-09-878-766A-2	-09-878-766A-	-07-928-462-1	8-273-24	-09-878-766A-1	-09-87	-08-961-527-	9-878-766A-	-08-961-083-53	-09-536-784-5	-09-878-766A-1	-107-532A-11	-09-134-000C-995	-09-134-001C-26	-08-956-171E-12	-09-134-000C-82	-09-107-532A-40	-08-545-52	-06906	-634-238-1	-09-674-826B-	-09-543-681A-391	-09-48	-09-489-039A-50	S-09-198-452A-1	-08-311-731A-12	-001C-9
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ALIGNMENTS

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RESULT 1
US-09-878-766A-21

Sequence 21, Application US/09878766A

Patent No. 6660270

GENERAL INFORMATION:

APPLICANT: Portaine, Michael

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

TITLE REFERENCE: 9000-0057

TILE REFERENCE: 9000-0057

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT PILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 1347

TYPE: DNA

ORGANISM: Artificial Sequence
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OTHER INFORMATION: chimeric GapC protein
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Query Match
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RESULT 2
US-09-878-766A-11
; Sequence 11, Application US/09878766A
; Patent No. 6660270
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Potter, Anchael
; APPLICANT: Fontaine, Michael
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAP(
; TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0057
; CURRENT APPLICATION NUMBER: US/09/878,766A
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
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Pred. No. 8.1e-215;
0; Mismatches 22;
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TCGATGGTACTGTAGAGTTAAAGAAGGTGGATTCGAAGTTAACGGTCAATTTGTTAAAG
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                                                                 HOD: experimental
/codon_start= 115
/function= "High-affinity binding of plasmin(ogen)"
/product= "Streptococcal plasmin rec/evidence= EXPERIMENTAL/gene= "plr"
/number= 1
/label= PLR
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Pred. No. 4.2e-205;
); Mismatches 44;
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nilarity 94.8%;
Conservative (
NAME/KEY: CDS
LOCATION: 115..1122
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 115..1122
IDENTIFICATION METHOD:
OTHER INFORMATION: /fun
OTHER INFORMATION: /pro
OTHER INFORMATION: /pro
OTHER INFORMATION: /gen
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CTGAAGATCCAATTGTTTCTTCAGATATCGTAGGCGTGTCATACGGTTCATTGTTTGACG
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                                               CATGGT
                                                                                                      caactcaaactaaagttarggaagtrgacegarcacaarregtraaagtretar
                                                                                                                                                                                                                                                                                                 APPLICANT: Boyle, Michael D.P.
APPLICANT: Boyle, Richard
APPLICANT: Lottenberg, Richard
APPLICANT: Lottenberg, Richard
APPLICANT: won Mering, Gregory O.
TITLE OF INVENTION: Bacterial Plasmin Receptors as
TITLE OF INVENTION: Fibrinolytic Agents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
JRRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,462
FILING DATE: 19920810
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R: UF/S&S-13.C2
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411
FILING DATE: 16-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,849
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus pyogenes
STRAIN: M untypable
INDIVIDUAL ISOLATE: 64/14
IMMEDIATE SOURCE:
CLONE: PRL015
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Patent No. 5328996
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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HYPOTHETICAL: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE:
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NAME/KEY: mat_peptide
LOCATION: 115..1122
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /codon_start= 115
OTHER INFORMATION: /function= "High-affinity binding
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: DATE: Ploppy disk
COMPUTER: DATE: PLOPS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WINBER: US/08/273,247
FILING DATE: 16-MX-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411
APPLICATION NUMBER: US 07/524,411
APPLICATION NUMBER: US 07/330,849
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, DATE:
APPLICATION NUMBER: 31,794
REFERBNCE/DOCKET NUMBER: 31,794
REFERBNCE/DOCK
                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08273247

Sequence 1, Application US/08273247

Patent No. 6136323

GENERAL INFORMATION:
APPLICANT: Boyle, Michael D.P.
APPLICANT: Lottenberg, Richard
APPLICANT: Lottenberg, Richard
APPLICANT: Broder, Christopher C.
APPLICANT: Apples September C.
APPLICANT: Agence Appress:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
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STRAIN: M untypable
INDIVIDUAL ISOLATE: 64/14
IMMEDIATE SOURCE:
CLONE: PRL015
                                                                                                               TCGCTAAATAA 1347
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MOLECULE TYPE: DN/
HYPOTHETICAL: NO
FRAGMENT TYPE: N-1
ORIGINAL SOURCE:
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LOCATION:
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US-08-273-247-1
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                                                           Length
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       plasmin
                                                          Score 780.6; DB 3;
Pred. No. 4.2e-205;
0; Mismatches 44;
plasmin(ogen)"
/product= "Streptococcal p
/evidence= EXPERIMENTAL
/gene= "plr"
/number= 1
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Local Similarity 94.8%;
nes 807; Conservative
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; OTHER INFORMATION:
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US-09-878-766A-13

US-09-878-766A-13

Sequence 13, Application US/09878766A

Patent No. 6660270

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Potter, Andrew A.

TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPITILE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

FILE REFERENCE: 9000-0057

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.5e-183;
0; Mismatches 93;
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Best Local Similarity 89.1%;
Matches 758; Conservative
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                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1)
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Sequence 19, Application US/09878766A;
Sequence 19, Application US/09878766A;
Patent No. 6660270;
GENERAL INFORMATION:
APPLICANT: Potter, Andrew A.
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: Michael
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 1011
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LOCATION: (1)
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Sequence 2, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides a
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                  ATGACAATGAAATGTCTTACACTGCTCAACTTGTTCGTACACTTGAGTATTTTG
CTGAAGATCCAATTGTTTCTTCAGATATCGTAGGCGTGTCATACGGTTCATTGT
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DAIE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7571 base pairs
TYPE: nucleic acid
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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA
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CLASSIFICATION: 424
IOR APPLICATION DATA:
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TOPOLOGY: linear
-961-527-2
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INFORMATION FOR
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7571;
Length
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Score 678.2; DB 4;
Pred. No. 1.6e-176;
); Mismatches 98;
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Patent No. 6660270
GENERAL INFORMATION:
APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
                        0;
Query Match
Best Local Similarity 88.1%;
Matches 750; Conservative
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APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
LENGTH: 1011
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Pred. No. 1.6e-176;
); Mismatches 109;
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Conservative (
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                                                                                                          NAME/KEY: CDS
LOCATION: (1)..(1011)
9-878-766A-15
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742; Conserv
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Best Local S
Matches 742
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TCGATGGTACTGTTGAAGTTAAAGGTGGATTCGAAGTTAACGGTCAATTTGTTAAAG
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                                                                                                                                                                           TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
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ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION SATA:
APPLICATION NUMBER:
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Pred. No. 5.3e-172;
); Mismatches 98;
                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36,373
ER: PB340P2
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; Sequence 53, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 87.9%;
Matches 743; Conservative
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nucleic acid
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REFERENCE/DOCKET NUMBER: PB340P3
            TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                             INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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ilarity 87.9%;
Conservative
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Local Sim:
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  CTGCAC
                                                                                                                                                                 CTGCAC
                                                                                                                                                                                                                                                                                                                         TTGACG
   GTACTA
                         CAAACTGTTTAGCTCCTATGGCTAAAGCTCTTCACGATGCATTTGGTATCCAAAAAGGTC
                                     ACCGTG
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ACACTAACCACGACGTTCTTGACGGTACTGAAACAGTTATCTCAGGTGCTTCAT
                                                                                                                                                              CTGCTAAAGCTATCGGTCTTGTTATCCCAGAATTGAATGGTAAACTTGATGGTG
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                                                                   TTATGACTACAATCCACGCTTATACTGGTGACCAAATGATCCT
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PE: Diskette, 3.50 inch, 1.4Mb
HP Vectra 486/33
SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 9410 Key West Avenue CITY: Rockville STATE: Marvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MSDOS version 6
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
NNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 53, Application US/09536784 Patent No. 6573082 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maryland
Y: USA
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                                                                                                 Gaps
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                                                                Length 1000;
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(3e-172;
(es 98;
                                                              Score 660.2; Pred. No. 5.3e.0; Mismatches
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-536-784-53
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CITY: W
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Sequence 1115, Ap
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                                                                Sequence 17, Application US/09878766A

Sequence 17, Application US/09878766A

GENERAL INFORMATION:
APPLICANT: Porter, Andrew A.
APPLICANT: Perez-Casal, Jose
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIL
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 1011
                                                                                                                                                                                                                                                                                                       Score 639.8; DB 4;
Pred. No. 2.2e-166;
0; Mismatches 132;
                                                                                                                                                                                                                                          ORGANISM: Streptococcus parauberis
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.5%;
Matches 719; Conservative
                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (1)..(1011)
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1340
                   996 ATTGC
1336 ATCGC
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US-09-878-766A-17
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                           1000
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                                             820
                                                                                                                                 880
                                                                                                                                                                      ATGACAATGAAATGTCTTACACTGCTCAACTTGTTCGTACACTTGAGTATTTTGCAAAAA
                                        cricagiagadaarraacreagraargaagereereeraargarrearargerraea
                                                                                       CTGAAGATCCAATTGTTTCTTCAGATATCGTAGGCGTGTCATACGGTTCATTGTTTGACG
                                                                                                              TITCTGTTGACGAAATCAACGCTGCTATGAAAGCTGCTTCAAACGACAGTTTCGGTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1002
SEQUENCE DESCRIPTION: SEQ ID NO: 1115:
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Patent No. 6583275
GENERAL INFORMATION:
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TER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPE
STREET: 100 Beaver Street
CITY: Waltham
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TELEFAX: (781)893-8277
MATION FOR SEQ ID NO: 1115:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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TCGCTAAATAA 1011
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ORIGINAL SOURCE
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                     Indels
5; DB 4;
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nes 204;
Score 495.6; I
Pred. No. 1.1e.
0; Mismatches
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Sequence 995, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FO

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13
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36.8%;
il Similarity 75.3%;
631; Conservative
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Matches 631
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   60/055,778
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                                                                                                                                                                                               ; ORGANISM: Enterococcus faecalis
US-09-134-000C-995
PRIOR APPLICATION NUMBER: US 60 PRIOR FILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTWARE: Patentin version 3.1 SEQ ID NO 995 LENGTH: 1041
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larity 74.0%;
Conservative
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RESULT 14 US-09-134-001C-2676

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aureus Polynucleotides and Sequences
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
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Pred. No. 1.6e-102;
0; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                             Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 6048 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 128:
                                                                                                                                                                                                                                            APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus au
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Scie
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                   Sequence 128, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
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Sequence 2676, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGN
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2676
LENGTH: 1047
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	equence 21, A	equence 11, App	ppl	Appl	, App	195 Sequence 38195, A	, App	13,	Н	5, App	Sequence 9495, Ap	19, App	App,	, Ap	
ID	.S-09-878-766	- 76	US-09-878-781-3	-134-2	-878-7	-282-122A-38		US-09-878-766A-13	급	0-134-297-	US-09-815-242-9495	US-09-878-766A-19	US-09-878-781-11	US-10-134-297-11	US-09-815-242-9071
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ALIGNMENTS

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APPLICANT: Potter, Andrew A.
APPLICANT: Potter, Andrew A.
APPLICANT: Potter, Anchael
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: MACHAEL
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 1347
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
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Best Local Similarity 100.0%; Pred. No. 2.6e-308;
Matches 1347; Conservative 0; Mismatches 0;
                             Sequence 21, Application US/09878766A Patent No. US20020044928A1 GENERAL INFORMATION:
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RESULT 1
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; NAME/KEY: CDS
; LOCATION: (1)..(1011)
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LENGTH: 1011
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; Sequence 3, Application US/09878181
; GENERAL INFORMATION:
; APPLICANT: Bolton, Alexandra J.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AG; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0055
; CURRENT APPLICATION NUMBER: US/09/878,781
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 18
                                                                                                        Length 1011;
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SOFTWARE: Patentin Ver.
SEQ ID NO 3
LENGTH: 1011
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Best Local Similarity
Matches 829; Conser
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Sequence 3, Application US/10134297
Bublication No. US20030165524A1
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
APPLICANT: Fontaine, Michael
APPLICANT: Forter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055.20
CURRENT APPLICATION NUMBER: US/10/134,297
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 9.7e-183;
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RESULT 5
US-09-878-13
; Sequence 13, Application US/098781
; Fublication No. US20030082781A1
; GENERAL INFORMATION:
; APPLICANT: Bolton, Alexandra J.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
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                                                                                                             Sequence: SpyGapC
                                                                                                                                            Length
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                                                                                                                                           Score 790.2; DB 10;
Pred. No. 1.1e-176;
); Mismatches 38;
                                                                                                           OTHER INFORMATION: Description of Artificial -09-878-781-13
             878,78
FILE REFERENCE: 9000-0055

CURRENT APPLICATION NUMBER: US/09/87

CURRENT FILING DATE: 2002-09-10

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 13

LENGTH: 961
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                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ilarity 95.5%;
Conservative
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Best Local Similarity
Matches 813; Conser
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; Sequence 15, Application US/09878781
; Sequence 15, Application US/09878781
; GENERAL INFORMATION:
; APPLICANT: Bolton, Alexandra J.
; APPLICANT: Portaine, Michael
; APPLICANT: Fontaine, Michael
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGA:
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0055
; CURRENT APPLICATION NUMBER: US/09/878,781
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1010
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Pred. No. 7.5e-174;
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ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 2e-174;
0; Mismatches 44;
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                                                                     Sequence 38195, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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Best Local Similarity 94.8%;
Matches 807; Conservative
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Score 702.2; DB 9;
Pred. No. 7.1e-156;
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FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 1011
TYPE: DNA
                                                TYPE: DNA
CRGANISM: Streptococcus agalactiae
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1011)
US-09-878-766A-13
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al Similarity 89.1%;
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US-09-878-766A-13
; Sequence 13, Application US/09878766A
; Patent No. US20020044928A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Potter, Michael
; APPLICANT: Fontaine, Michael
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH
; TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
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Pred. No. 7.1e-156;
0; Mismatches 93;
                                                                   Sequence 5, Application US/09878781
; Publication No. US20030082781A1
; GENERAL INFORMATION:
; APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
, APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CP; TITLE OF INVENTION: STREPTOCOCCUS INFECTION FILE REFERENCE: 9000-0055
; CURRENT APPLICATION NUMBER: US/09/878,781
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
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; LOCATION: (1)..(1011)
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Publication No. US20030165524A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
APPLICANT: Portaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055.20
CURRENT APPLICATION NUMBER: US/10/134,297
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
701 AACGTGTTCCTGTTCCAACTGGATCAGTAACTGAATTGGTTGCAACTCTTGAAAAAGACG
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                                     TTTCTGTTGACGAAATCAACGCTGCTATGAAAGCTGCTTCAAACGACAGTTTCGGTTACA
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Pred. No. 7.1e-156;
); Mismatches 93;
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llarity 89.1%;
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LOCATION: (1)..(1011)
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CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of ESTITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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Pred. No. 2.5e-151;
); Mismatches 95;
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                           TYPE: DNA
CRGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1080)
US-09-815-242-9495
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Local Similarity 88.5%;
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             Sequence 19, Application US/09878766A

Sequence 19, Application US/09878766A

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Perez-Casal, Jose

APPLICANT: Fontaine, Michael

TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHI

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

FILE REFERENCE: 9000-0057

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 19

LENGTH: 1011
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Pred. No. 3.4e-150;
0; Mismatches 108;
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Best Local Similarity
Matches 743; Conser
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LOCATION: (1)
S-09-878-766A-19
RESULT 12
US-09-878-766A-19
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Sequence 11, Application US20030082781A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
APPLICANT: Ferez-Casal, Jose
APPLICANT: Perez-Casal, Jose
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILLE REFERENCE: 9000-0055
CURRENT APPLICATION NUMBER: US/09/878,781
CURRENT FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 3.4e-150;
); Mismatches 108;
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Best Local Similarity 87.3%;
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patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Young T.
APPLICANT: Yamamoto, Yamamot
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APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
APPLICANT: Fotter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEI
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Pred. No. 3.4e-150;
); Mismatches 108;
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CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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Publication No. US20030165524A1
GENERAL INFORMATION:
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Pred. No. 3.5e-150;
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 9071
                                                                                                                                                     ORGANISM: Streptococcus pneumoniae FEATURE:
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Best Local Similarity 88.1%;
Matches 750; Conservative (
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; LOCATION: (1)...(1080)
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ACAATTGGTTAA ACAATTGGTTAA	CGTACACTTG	
TTGACGGATCA TTGACGGTAAA	CTCAACTIGII CACAACTIGII	
AGTTATGGAAG AGTTCTTGACG	GTCTTACACTG 	347
1217 CAACTCAAACTAAAGTTATGGAAGTTGACGGATCACAATTGGTTAAAGTTGTATCATGGT 1276 	1277 ATGACAATGAAATGTCTTACACTGCTCAACTTGTTCGTACACTTGAGTATTTTGCAAAA 1336	1337 TCGCTAAATAA 1347 1070 TTGCTAAATAA 1080
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Search completed: March 31, 2004, 03:18:54 Job time : 509 secs

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Description	BH770540 LLMGtag CB686102 Bn01b 0 AF075927 AF07592 CK261340 EST7074
QI	BH770540 CB686102 AF075927 CK261340
DB	12128 1284 1484
ngth	1127 990 944 973
% Query Matcl	8444 0.444 0.446
Score	471.8 195.6 190.6 189
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28 AZ536323	2 BI43394	4 CK27693	4 CK27233	4 CK27282	AI77926	2 BI42298	0 AW2671	AI782605	2 BQ04582	4 CA83555	8 BH15871	2 BG5909	AW096431	8 AZ69219	4 CA83622	4 CA83628	4 CA83598	2 BJ40099	2 BJ39805	2 BJ37415	2 BJ39833	AU039919	4 CA83685	0 AW77556	3 BQ70489	2 BJ38406	AU060734	AW09369	2 BJ39970	2 BM3000	2 BI94577	2 BM41138	2 BG45214	AW09650	2 BJ43030	0 BE1306	2 BG45215	2 BG26889	4 CK26091	ATT062136	1
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ALIGNMENTS

BH770540 linear GSS 01-MAY-2002 UNITION LLMGtag303 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, genomic survey sequence.

ESSION BH770540.1 GI:20373497

WORDS GSS.

Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.

Lacto

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                                                                      /sub_species="cremoris"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGMU2; Site_1: Smal; Library of chromosomal fragments of L. lactis strain MG1363 prepared by partial AluI digestion or by sonical
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                                                                                                                                                                                                Length 1127
                               cremoria
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                              subsp.
                                                                                                                                                                                                Score 471.8; DB 28;
Pred. No. 1.1e-110;
); Mismatches 227;
                               lactis
                            organism="Lactococcus
mol_type="genomic DNA'
strain="MG1363"
Location/Qualifier
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larity 73.0%;
Conservative
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621; Conser
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Best Local S
Matches 621
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/clone="Bn01b 02m19"
/tissue_type="fourth leaf"
/dev_stage="3 weeks seedling grown at room temperature"
/dev_stage="3 weeks seedling grown at room temperature"
/clone_lib="Bn01b_AAFC_ECORC_transgenic_Brassica_napus_ove
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/note="Vector: Bluescript_SK+/XhoI-EcoRI; Site_1: EcoRI;
/note="Vector: Bluescript_SK+/XhoI-EcoRI; Site_1: EcoRI;
Site_2: XhoI; Germinated in soil flats and seedlings grown
for 3 weeks in a Conviron E-15 cabinet set at 20oC /16 hr
light (250 Em-2sec-1) and 16 oC / 8 hr dark. Fourth leaves
collected at 9 am and immediately frozen."
                                                                                                                                          CB686102

Bn01b 02m19 A

Bn01b AAFC ECORC transgenic Brassica napus overexpressing BNCBF17 constitutively frost tolerant Brassica napus cDNA clone Bn01b 02m19, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 990)
Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A., Chagnon,J., Farah,S., Couroux,P. and Hattori,J.

Expressed Sequence Tags from constitutively frost tolerant transgenic Brassica napus overexpressing BNCBF17
Unpublished (2002)
Contact: Singh,J.A.

Eastern Cereal and Oilseed Research Centre
                                                                                                                                      09-APR-2003
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KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KlA
OC6, Canada
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Pred. No. 2.5e-39;
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cultivar="Westar"
db_xref="taxon:3708"
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1. .990
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Fax: (613) 759-1701
Email: singhja@em.agr.ca
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/note="Vector: Lambda DASH II; sequenced using Li-Cor
sequencer"
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AF075927 Salmonella typhimurium LT2, Lambda DASH I typhimurium genomic clone B159-T7, genomic survey AF075927
AF075927.1 GI:3320797
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Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Salmonella.
1 (bases 1 to 944)
Wong, R.M.-Y., Wong, K.K., Benson, N.R. and McClel
Sample sequencing of a Salmonella typhimurium L
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strain="LT2"
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Molecular Biology
Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego,
Email: mcclelland@lifsci.sdsu.edu
Class: shotgun.
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Length 944;
   Score 190.6; DB 28; Length
Pred. No. 4.8e-38;
); Mismatches 314; Indels
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KEYWORDS
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// Liste From Day 2.

// Lab host="Day 100 - TonA"

// Lab host="Day 100 - TonA"

// Lab host="Day 100 - TonA"

// Clone lib="potato abiotic stress cDNA library"

// Clone lib="potato abiotic stress cDNA library"

// Note="Vector: pCMVSport6.1; Site 1: BCORI; Site 2: Not1;

supplier: Sclanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25

C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."
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                                                      Tracheophyta
Solanum tuberosum (potato,

Solanum tuberosum

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Solanum.

E 1 (bases 1 to 973)

S Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

Generation of ESTs from abiotic stressed potato tissue

L Unpublished (2003)

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                /organism="Solanum tuberosum"
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAB929"
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Matches 432
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/mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Institute for Genomic Research cultures of E. histolytica Genomic DNA isolated from broth cultures of E. histolytica
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                   GGTGCTGCAAACATTGTTCCTAACTCAACTGGTGCTGCTAAAGCTATCGGTCTTGTTATC
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Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 892)
1 (bases 1 to 892)
2 Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytic HM1: IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1: IMSS she
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Entamoeba histolytica"
'mol tvpe="genemic ....
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Class: shotgun
High quality sequence start: 38
High quality sequence stop: 843.
Location/Qualifiers
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using a method described by Clark and Diamond (Clar) C.G., and Diamond, L.S. (1993) Entamoeba histolytics method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method use the library construction is described in detail in the library construction is described in detail in the No. and Venter, J.C. (Making small insert libraries whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barell, Oxford University Press, 1999)."
                                                               rve a
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.

E 1 (bases 1 to 772)
S Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B. Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction

L Unpublished (2000)
Contact: Robin Buell
The Institute (2000)
Contact: Robin Buell
The Institute of Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seg primer: M13F-R.
Location/Qualifiers
1. .772
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XhoI; supplier: Cornell University, Fry lab; sequencing:
The Institute for Genomic Research; Whole plants were
challenged with 20,000 sporangia/ml of the compatible P.
infestans isolate US 940480. Leaf tissue was collected at
3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen
in liquid nitrogen immediately upon removal. Kennebec
plants showed first symptoms of infection at 48 hours
after inoculation. NOTE: We cannot exclude the
possibility that this sequence is actually derived from
Phytophthora rather than potato."
                                                                                                                            B1433946
EST536707 P. infestans-challenged potato leaf, compatible reaction Solanum tuberosum cDNA clone PPCBK36 5' sequence, mRNA sequence.
B1433946.1 GI:15258636
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/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PPCBK36"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="Solk"
/clone_lib="P. infestans-challecompatible reaction"
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nilarity 55.6%;
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Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Track
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
asterids; lamiids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 955)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Bake
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST723016
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
CK276937

EST723015 potato abiotic stress cDNA library Solanum tub clone POADW68 5' end, mRNA sequence.
CK276937
CK276937.1 GI:39833915
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        via potato@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                Email: potato-array@tigr.org
Clones can be requested from TIGR vi
Seg primer: ATT TAG GTG ACA CTA TAG
Location/Qualifiers
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host="DH10B-TonA"
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cultivar="Kennebec"
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/tissue_type="abigate"/lab_host="DH108-"
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TITLE
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/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pcMvSport6.1; Site_1: EcoRI; Site_2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM Nacl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d, roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d, roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to

1182 1002 882 582 642 379 822 583 ATTGACTGGGCTACTGATGGCGTAGAAATCGTTCTTGAAGCAACTAGTTTCTTTGCTAAA ccagaarregarageraagerregregrecregaaceregregregregregregarea GTTGTGGACCTTGTCGTTCAAGTCACCAAGAGACATTTGCTGAGGAAGTGAATGCTGCA 763 ACTGAAACAGTTATCTCAGGTGCTTCATGTACTACAAACTGTTTAGCTCCTATGGCTAAAA GGTGCTGCAAACATTGTTCCTAACTCAACTGGTGCTGCTAAAGCTATCGGTCTTGTTATC GTAACTGAGTTGGTTAACTCTTGATAAAACGTTTCTGTTGACGAAATCAACGCTGCT 523 GGTGGATTCGAAGTTAACGGTCAATTTGTTAAAGTTTCTGCTGAACGCGAACCAGCAAAC 440 gardakactrarckreaceantecererreckeekeekeidecerrecreereka GCTCTTCACGATGCATTTGGTATCCAAAAGGTCTTATGACTACAATCCACGCTTATACT 560 gereacchadecrircricarecaaccacaes-----carcriagacerecaeger 614 gcagcarrgaacaradrrccaaccrcaacrcadrordcrocraagcrargacrcric ATGAAAGCTGCTTCAAACGACAGTTTCGGTTACACTGAAGATCCAATTGTTTCTTCAGAT 203 gardgaarcrerereadeaaaaaarcarceaadreerereeaceaceaaces 263 CTCCCATGGGGGGAACTTGGATTTGGTCATAGAAGGTACCGGAGTGTTTGTAGAC ccceeaaaaggreararccractrarerrargreergreaargcreaacritacaaccar GGTGACCAAATGATCCTTGACGGACCACACCGTGGTGGTGACCTTCGTCGTGCTCGTGCT CCTGGTGGAAACGACGTTAAAACAGTTGTTTTCAACACTAACCACGACATTCTTGACGGT Gaps 12; Score 181.6; DB 14; Length 955; Pred. No. 1e-35; 0; Mismatches 329; Indels 12; 0 13.5%; Similarity 55.2%; 11; Conservative (421; 1063 500 943 323 703 Query Match Best Local (Matches qq g а g Д a පු d 원 ઠે ਨੇ 8 8 à ਨੇ ਨੇ ð ઠે ਠੇ

TTCAGAGAAGCTGCTGATAAGGAACTCAATGGCATTCTAGCTGTCTGCGATGAACCACTT

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us-10-650-369-21

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CK272824

EST718902 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAD755 5' end, mRNA sequence.

CK272824

CK272824.1 GI:39829802
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Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopl
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 973)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B
Generation of ESTs from abiotic stressed potato tissue
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Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850,
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ON EST718408 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAD453 3' end, mRNA sequence.

OK272330.

CK272330.1 GI:39829308

CK2723330.1 GI:39829308

CK2723330.1 GI:39829308

CK272330.1 GI:39829308

Solanum tuberosum (potato)

SM Solanum tuberosum (potato)

Authoritis lamids; Solanales; Solanaceae; Solanum.

CGeneration of ESTS from abiotic stressed potato tissue

Authoritished (2003)

Contact: Robin Buell

The Institute for Genomic Research

SM Solanum tuberosum (potato@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
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/organism="Solanum tuberosum"
/mol type="mRNA"
/culfivar="Kennebec"
/db xref="taxon:4113"
/clone="PoAD453"
/tissue type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-TonA"
/clone=lib="potato abiotic stress cDNA library"
/clone=lib="potato abiotic stress cDNA library"
/clone=lib="potato abiotic stress cDNA library"
/clone=lib="potato abiotic stress conditions were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
c for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM Nacl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; rootesiahr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 3d, and 7d, roots: 3d
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
atressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
atressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and heat-stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."
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313;
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              n TIGR via potato@tigr.org
CTA TAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.2%; Score 178.2; DB 14; larity 58.3%; Pred. No. 7.7e-35; Conservative 0; Mismatches 243;
                                                                    organism="Solanum tuberosum"
                                                                                             "cultivar="Kennebec"
'db_xref="taxon:4113"
'clone="POAD755"
Email: potato-array@tigr.org
Clones can be requested from
Seg primer: ATT TAG GTG ACA (
                                      Location/Qualifiers
                                                                                 type="mRNA"
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

(bases 1 to 641)

Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,

Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y.,

Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,

Giovannoni,J.J. and Martin,G.B.

Generation of ESTs from Pseudomonas susceptible tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        582
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EST260146 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES7N21, mRNA sequence.
AI779267
AI779267.1 GI:5277308
EST.
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  CCAGAATTGAATGGTAAACTTGATGGTGCTGCACAACGTGTTCCTGTTCCAACTGGATCA
                                           GIBACTGAGTTGGTTATAACTCTTGATAAAACGTTTCTGTTGACGAAATCAACGCTGCT
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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/mol_type="mRNA"
/cultivar="Ril-13 (Rio Grande x Money Maker)
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clone="cLES7N21"
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Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"

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GTAACTGAGTTGTAACTCTTGATAAAACGTTTCTGTTGACGAAATCAACGCTGCT 1122
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                                                                                523 GGTGGATTCGAAGTTAACGGTCAATTTGTTAAAGTTTCTGCTGAACGCGAACCAGCAAAC
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Gastric associated differentially expressed gene mRNA sequence
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Homo Bapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eucharyota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 530)
1 (bases 1 to 530)
2hao, J.R., Yan, X.J., Han, F.C., Cui, D.X., Hou, Y., Yan, Q.J. and zhao, J.R., Yan, X.J., Han, F.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Zhao JR
Institute of Genetic Diagnosis, the Fourth Military Medical
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YA61 gastric carcinoma cell GC7901 Homo sapiens cDNA, mRNA sequence.
AW26/163
AW26/163.1 GI:664/328
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   DB 12; Length 783;
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                                           247;
Score 177.8; DE
Pred. No. 9e-35;
0; Mismatches 2
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58.1%;
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                                                                                                                                                                                                                                       /organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="gastric carcinoma cell GC7901"
/clone_lib="gastric carcinoma cell GC7901"
/note="differentially expressed gene sequences from hugastric carcinoma cell GC7901 . The method used is gastric carcinoma cell GC7901 . The gastric epithelial
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Pred. No. 2.9e-34;
); Mismatches 189;
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xi'an, China, 710032
Tel: 86 029 3374771
Email: Zhaojr@263.net
Seg primer: M13 Forward
POLYA=Yes.
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larity 61.0%;
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18-MAY-2001
                                                                                                                                          Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 626)
                                                     entum cDNA
                                   EST
                                                       eacu
AI782605
EST263484 tomato susceptible, Cornell Lycopersicon
clone cLES20I13, mRNA sequence.
AI782605
AI782605.1 GI:5280646
                                                          DEFINITION
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                       REFERENCE
                     AI782605
   RESULT
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471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="tomato susceptible, Cornell"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2
Xhol; cles - Tomato Pseudomonas Susceptible EST Library
Directionally cloned cDNAs inserted into pBlueScript
SK(-) at 5' end with EcoRI and 3' end with Xhol site"
                                   Holt, I.E
D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.! Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D. Giovannoni, J.J. and Martin, G.B. Generation of ESTs from Pseudomonas susceptible tomato Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 ATCAGCAATGCCTCTTGTACCACCAACTGCCTTGCTTCCTTTCGTCAAGGTTCTTGACCAG
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                                                                                                                                                                                                               Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                          'organism="Lycopersicon esculentum"
'mol_type="mRNA"
'cultivar="R11-13 (Rio Grande x Money Maker)
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                                                                                                                                                                                             Clemson University Genomics Institute
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dev_stage="4-week old"
lab_host="SOLR"
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clone="cLES20113"
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                                                                                                                                      Solanum tuberosum (potato)
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.

I (bases 1 to 771)
S Zhang, P., Hernandez, M., Tornqvist, C.-E., Wirtz, U., Loukoianov, A., Rangel, P., Haberlach, G.T., Karamycheva, S.A., Tsai, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.M., Helgeson, J. and Baker, B.
Generation of ESTS from Potato Leaves Challenged with Phytophthora infestans, incompatible Interaction (2002)
Unpublished (2002)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3:
                                 10-MAR-2003
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3-1) were
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/dev_stage="leaf"
/dev_stage="leaf"
/dev_stage="leaf"
/lab_host="SOLR"
/clone_lib="P. infestans-challenged potato leaf,
incompatible reaction"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site
XhoI; supplier: UC Berkeley, PGEC; sequencing: The
Institute for Genomic Research. Whole plants were
challenged with 450,000 sporangia/ml P. infestans isc
US-1 (US940501) in Biotron (Madison, Wisconsin). Leaf
tissue was collected at 1, 2, 5, 12, and 24 hours
post-challenge and frozen in liquid nitrogen immediat
upon removal. Kennebec plants showed no signs of HR.
Katahdin plants (susceptible to P. infestans US-1) we
used as controls and showed infection. NOTE: We cann
exclude the possibility that this sequence is actual
derived from Phytophthora rather than potato. ".
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                             771 bp mRNA linear EST 34 P. infestans-challenged potato leaf, incompatil solanum tuberosum cDNA clone BPLI13A7 5' end, m
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Pred. No. 8.6e-34;
); Mismatches 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Solanum tuberosum"
/mol_type="mRNA"
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="BPLI13A7"
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Location/Qualifiers
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Best Local S
Matches 426
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RESULT 14
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CA835550
MCS038C08 160608 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS038C08 5, mRNA
                                                                                                                                                                                                                                                                                                                                                                                            1002
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Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                        416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGAATTGAATGGTAACTTGATGGTGCTGCACAACGTGTTCCTGTTCCAACTGGATCA
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An expressed sequence tag database for the common ice plant
Mesembryanthemum crystallinum
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1238 AAGTTGACGGATCACAATTGGTTAAAGTTGTATCATGGTATGACAATGAA 1287
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Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, U
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
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Plate: 038 row: C column:
Seg primer: T3 20mer
High quality sequence stop:
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r7 21mer
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Location/Qualifiers

1. .698
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/dlone="MCS038C08"
/tissue_type="leaf"
/clone_type="leaf"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: Xhol; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."
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Search completed: March 31, 2004, 01:55:47 Job time : 3354 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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- protein search, using sw model OM protein March 29, 2004, 15:57:18; Search time 96.4776 Seconds (without alignments) 1312.028 Million cell updates/sec Run on:

1 MKKITGIILLLLAVIILSAC......EMSYTAQLVRTLEYFAKIAK US-10-650-369-22 2278 score: ritle: Perfect

448

table: Sequence: Scoring

282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 1586107 segs, Searched:

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Database

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1: geneseqp1980s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Streptococcus GapC multiepitope fusion PolyGap4
      AAM50664 standard; protein; 448 AA.
                  (revised)
(first entry)
                 29-AUG-2003
08-APR-2002
            AAM50664;
RESULT 1
AAM50664
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PolyGap4; GapC; plasmin binding protein; epitope; infection; vaccine; immunisation; mastitis; therapy.

dysgalactiae. s agalactiae. s parauberis. Streptococcus Streptococcus Streptococcus Chimeric

WO200196379-A2.

20-DEC-2001.

2001WO-CA000836. 2000US-0211247P. (UYSA-) UNIV SASKATCHEWAN. 12-JUN-2000; 11-JUN-2001;

Fontaine M; Perez-Casal WPI; 2002-098051/13. N-PSDB; ABA91327. Potter AA,

S Novel GapC multiple epitope fusion polypeptide comprising antigenic determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, parauberis, or S. iniae GapC protein useful for treating mastitis in vertebrates.

Claim 9; Fig 6A-C; 116pp; English.

The present sequence is that of a novel multiple epitope fusion protein, designated PolyGap4, comprising the entire amino acid sequence of the Streptococcus dysgalactiae GapC plasmin binding protein in addition to unique amino acid sequences from the Streptococcus parauberis and Streptococcus agalactiae GapC proteins. The multiple epitope protein is produced in host cells transformed with an expression vector comprising a produced in host cells transformed with an expression vector comprising a chimeric gene (see ABA91327) encoding the protein. PolyGal4 is an example

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of novel GapC multiple epitope fusion proteins of the invention that comprise epitopes from 1 or more of S. dysgalactiae, S. agalactiae, S. parauberis, Streptococcus uberis and Streptococcus iniae (see AAM50665-69). The multiple epitope fusion proteins are used in claimed vaccines for treating or preventing a bacterial infection in a vertebrate, especially a streptococcal infection, and particularly mastitis. They are also used in claimed methods of detecting Streptococcus antibodies. The multiple epitope protein is capable of eliciting broad immunity against variety of streptococcal infections while minimising the number of antigens present in the final formulation and concomitantly reducing production costs. (Updated on 29-AUG-2003 to standardise OS field)
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The present sequence is that of the GapC plasmin binding protein,

DysGapC, of Streptococcus dysgalactiae ATCC 43078, an isolate from a case
of bovine mastitis. The invention relates to novel GapC multiple epitope
fusion proteins that comprise epitopes from 1 or more of Streptococcus
c dysgalactiae, Streptococcus agalactiae, Streptococcus parauberis,
c streptococcus uberis and Streptococcus iniae (see AAM50665-69). A claimed
example is PolyGap4 (see AAM50664). Expression vectors and host cells for
production of the multiple epitope fusion proteins are provided. The
multiple epitope proteins are used in claimed vaccines for treating or
preventing a bacterial infection in a vertebrate, especially a
streptococcal infection, and particularly mastitis. They are also used in
c claimed methods of detecting Streptococcus antibodies. The multiple
epitope proteins are capable of eliciting broad immunity against a
variety of streptococcal infections while minimising the number of
antigens present in the final formulation and concomitantly reducing
production costs
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                                                                                                                  Novel GapC multiple epitope fusion polypeptide comprising antigenic determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, parauberis, or S. iniae GapC protein useful for treating mastitis in vertebrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 336;
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Pred. No. 4.9e-129;
); Mismatches 1;
                                              Fontaine M;
                                                                                                                                                                                                    116pp; English.
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nilarity 79.6%;
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                                              Perez-Casal
                                                                           2002-098051/13
                                                                                                                                                                                                        Claim 8; Fig 1A-B;
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Best Local Similarity
Matches 335; Conser
                                                                                            N-PSDB; ABA91328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated GapC protein of Streptococcus dysgalactiae, S.agalactiae, S.uberis, S.parauberis, or S.iniae, useful as vaccine component for treating streptococcal infection which causes mastitis in vertebrates.
                                                                                                                               plasmin-binding protein; DysgalGapC; infection; mastitis
                                                                                                  Streptococcus dysgalactiae gapC plasmin binding protein.
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standard; protein;
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                                                                                                                                                                                   Streptococcus dysgalactiae
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                                                                  (first
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N-PSDB; ABA91248.
                                                                                                                                                   diagnosis; therapy
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AAM50639
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Score 1656.5; DB 5;
Pred. No. 4.9e-129;
); Mismatches 1;
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11 Similarity 79.6%;
335; Conservative
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  Query Match
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and activity. (I), nucleic acids encoding (I), are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. (Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying

Streptococcus proteins

Sequence 336 AA;

Claim 1; Page 4031; 4525pp; English.

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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                            New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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N-PSDB; ABN70591.
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Tettelin H;
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                                      28 MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRF
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Score 1655.5; DB 5;
Pred. No. 5.9e-129;
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2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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                    1;
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ch 72.7%;
1 Similarity 79.3%;
334; Conservative
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N-PSDB; ACA50325.
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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The invention relates to an isolated nucleic acid comprising any one of the 6113 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a call. Also included are: of the nucleic acid, inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an best cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting fellular proliferation or the activity of a gene in an operon required for the activity of proliferation or that inhibits cellular proliferation; (7) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation; (8) required for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the strains is present in a culture or collection of product is overexpressed or underexpressed; (12) determining the extent proliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational derivative proliferation in organism. The arguence is encoded by one of the present did not form part of the sequence is encoded by one of the target prokaryoric essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the sequence is obtained.
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cellular proliferation to
                        rational drug discovery programs
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Pred. No. 5.9e-129;
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                                                                                 Claim 25; SEQ ID NO 74379; 1766pp; English
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   for homologous nucleic acids recisolate candidate molecules for
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334; Conservative
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KEGGFEVNGNFIKVSAERDPE
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90US-00524411.
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N-PSDB; AAQ70705.
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22-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

C Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying chromatography, immunoassays, and distinguishing/identifying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                                                                                                                                                                                 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agroup A streptococcus; Streptococcus proup A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
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Pred. No. 6.1e-129;
1; Mismatches 1;
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                                                                                                                                                                    Streptococcus polypeptide SEQ ID NO 7388
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                                                                         ABP29106 standard; protein; 345
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2000GB-00028727
2001GB-00005640
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24-NOV-2000;
07-MAR-2001;
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rettelin H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA encoding bacterial plasmin receptor - useful as thrombolytic agents, used with plasminogen activator or bound to plasmin, also useful in vaccines against bacterial infection.
                                                                  -- NIDWATDGVEIVLE
                                                                                                                                                                                       ATGFFAKKEAAEKHLHANGAKKVVITAPGGNDVKTVVFNTNHDILDGTETVISGASCTTN
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                                                       (Updated on
plasminogen activator (PA) so allows a reduction in dose, and thus lower the risk of bleeding, and may prevent reocclusion of blood vessels. The protein may be coupled to a fibrin-specific monoclonal antibody to provide targetting to clots. The plasmin receptor may be useful in human or veterinary medicine, for treatment of thrombosis and pulmonary embolism, and for solubilising clots in catheters or shunts. (Updated or 25-MAR-2003 to correct PF field.)
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Local Similarity 79.1%;
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10-AUG-1992;
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                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                       Polynucleotide sequence AAC66140 encodes the Streptococcal plasmin receptor protein AAY85681. The protein is used in a method for raising immune response in a mammal. The method comprises administering the plasmin receptor protein. The method is useful as a vaccination against group A Streptococcal infections and potentially against a broad range infections associated with pathogens expressing glyceraldehyde-3-phosphate dehydrogenase (GAPDH) or GAPDH-like proteins at their cell surfaces. The vaccine has antibacterial and antihelminthic activity
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                                                                     Against group A streptococcal infections, comprises administering a solated streptococcal infections, comprises administering assolated streptococcal plasmin receptor protein.
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                                                                                                                                                                                                                                                                                                           Length 336;
                                                                                                                                                                                                                                                                                                                                      Indels
           Boyle MDP
                                                                                                                                                                                                                                                                                                        Score 1652.5; DB 4;
Pred. No. 1e-128;
2; Mismatches 1;
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           Lottenberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEGGFEVNGNFIKVSAERDPB----
                                                                                                                                    Claim 2; Col 27-30; 17pp; English
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                                                                                                                                                                                                                                                                                                            72.5%;
79.1%;
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                                      2001-006210/01.
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                                                     N-PSDB; AAC66140.
                                                                                                                                                                                                                                                                                    Sequence 336 AA;
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             Von Mering
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                                                                                                                                                                                                                                                                                                      Query Mar.
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                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity, (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to detectmine whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                             fection or
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                                                                                                                                                                                                                                                                                                                                            and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85;
                                                                                                                                                                                                                                                                                                                         New Streptococcus protein for the treatment or prevention of disease caused by Streptococcus bacteria, such as meningitis, detecting a compound that binds to the protein.
                                                                                                                                                                                                                                 Fraser
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                                                                                                                                                                                                                                Margarit Y RosI,
                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 4179; 4525pp; English
                                                                                                                     2000GB-00026333.
2000GB-00028727.
2001GB-00005640.
                                                                                           2001WO-GB004789
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GENOMIC RES
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Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus proteins
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N-PSDB; ABN71389.
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INST GE
                             WO200234771-A2
                                                                                                                     27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
                                                                                           29-OCT-2001;
                                                           02-MAY-2002
                                                                                                                                                                                                                                 Telford J,
Tettelin H;
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Best Local
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(GENO-)
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The present sequence is that of the GapC plasmin binding protein,

UberGapC, of Streptococcus uberis ATCC 9927. The invention relates to

novel GapC multiple epitope fusion proteins that comprise epitopes from 1

or more of Streptococcus dysgalactiae, Streptococcus agalactiae,

creptococcus parauberis, Streptococcus uberis and Streptococcus iniae

Streptococcus parauberis, Streptococcus uberis and Streptococcus iniae

(see AAMSO665-69). A claimed example is PolyGap4 (see AAMSO664).

Expression vectors and host cells for production of the multiple epitope

(see AAMSO665-69). A claimed example is PolyGap4 (see AAMSO664).

Expression vectors and host cells for production of the multiple epitope

(claimed vaccines for treating or preventing a bacterial infection in a

vertebrate, especially a streptococcal infection in an astitis. They are also used in claimed methods of detecting

Streptococcus antibodies. The multiple epitope proteins are capable of

eliciting broad immunity against a variety of streptococcal infections

while minimising the number of antigens present in the final formulation

and concomitantly reducing production costs
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                                                                                                  216 KAIGLVIPELNGKLDGAAQRVPVPTGSVTELVATLEKDVTVEEVNAAMKAAANDSYGYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GapC; plasmin binding protein; epitope; infection; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85;
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llarity 73.9%; Pred. No. 5.5e-121;
Conservative 15; Mismatches 10;
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                                                                                                                                                                                                                 DPIVSSDIVGVSYGSLFDATOTKVMEVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIA
                                                                                                                                                                                                                                                           KAIGLVIPELNGKLDGAAQRVPVPTGSVTELVVTLDKNVSVDEINAAMKAASNDSFGYTE
  GTVEV
                       KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEALEGTVEVKDGGFDVNGKFIKVSAE
                                                                                                                             CLAPMAKALHDAFGIOKGLMTTIHAYTGDQMILDGPHRGGDLRRARAGAANIVPNSTGAA
                                                                                        -NIDWATDGVEIVLE
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  MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFI
                                                                                                             ATSFFAKKEAAEKHLHANGAKKVVITAPGGNDVKTVVFNTNHDILDGTETVISG
                                                                                                                                                                    148 KDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGOFVKVSAEREPANIDWATDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          gapC plasmin binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmin-binding protein; UberGapC;
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                                                                                                                                                                                                                                                                                                                                                                          AAM50641 standard; protein; 336 AA.
                                               KDGGFEVNGNFIKVSAEKDPE
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N-PSDB; ABA91250.
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compositions comprising GapC polynucleotides or proteins. The vaccines are used to treat or prevent a bacterial infection, especially a streptococcal infection, and mastitis in particular (claimed). GapC proteins are also used in claimed methods for detecting GapC antibodies, and to raise antibodies that are used in claimed methods for detecting GapC proteins. S. uberis is a common pathogen associated with mastitis is cattle, horse, sheep and goat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 KAIGLVIPELNGKLDGAAQRVPVPTGSVTFLVVTLDKNVSVDFLNAAMKAASNDSFGYTF
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                                                                                                                                                                                               85;
                                                                                                                                                                    Length 336;
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                                                                                                                                                                  DB 5;
                                                                                                                                                                  Score 1559.5; DB 5. Pred. No. 5.5e-121; 5; Mismatches 10;
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311; Conser
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The present sequence is that of the GapC plasmin binding protein,
AgalGapC, of Streptococcus agalactiae ATCC 27541. The invention relates
to novel GapC multiple epitope fusion proteins that comprise epitopes
C trom 1 or more of Streptococcus describes, Streptococcus agalactiae,
C streptococcus parauberis, Streptococcus uberis and Streptococcus iniae
C see AAMSO665-69). A claimed example is PolyGap4 (see AAMSO664).
C Expression vectors and host cells for production of the multiple epitope
C fusion proteins are provided. The multiple epitope proteins are used in
c claimed vaccines for treating or preventing a bacterial infection in a
C vertebrate, especially a streptococcal infection in a
C vertebrate, especially a streptococcal infection in a
C streptococcus antibodies. The multiple epitope proteins are capable of
C streptococcus antibodies. The multiple epitope proteins are capable of
C streptococcus infections
C streptococcus infections
C claimed vaccing broad immunity against a variety of streptococcal infections
C and concomitantly reducing production costs
                                                                                            Novel GapC multiple epitope fusion polypeptide comprising antigenic determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, parauberis, or S. iniae GapC protein useful for treating mastitis in
                                                                                                                                                                                                                                 Claim 8; Fig 2A-B; 116pp; English
                    WPI; 2002-098051/13
N-PSDB; ABA91329.
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Sequence 336 AA;

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                                                28 MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFD
                                                            1 MVKVGINGFGRIGRLAFRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRF-
                                                                                                88 KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEALEGTVEVKDGGFDVNGKFI
                                                                                                                                                148 KDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGQFVKVSAEREPANIDWATDGV
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68.4%; Score 1557.5; DB 5, larity 73.9%; Pred. No. 8.1e-121; Conservative 15; Mismatches 10;
            Similarity
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336
                    AAM50640 standard; protein;
                                                                  (first entry)
                                                                  04-APR-2002
                                           AAM50640;
         AAM50640
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KAIGLVIPELNGKLDGAAQRVPVPTGSVTELVVTLDKNVSVDEINAAMKAASNDSFGYTE

CLAPMAKALHDAFGIQKGLMTTIHAYTGDQMILDGPHRGGDLRRARAGAANIVPNSTGAA

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The present sequence is that of the GapC plasmin binding protein

(AgalGapC) of Streptococcus agalactiae ATCC 27541, encoded by the GapC

gene given in ABA91249. GapC, which has no signal sequence or membrane

c anchor domain, is capable of eliciting an immune response in a

vertebrate. The invention provides the GapC genes and proteins of 5

c streptococcus species, as well as recombinant vectors, host cells and

vaccine compositions comprising GapC polynucleotides or proteins. The

vaccines are used to treat or prevent a bacterial infection, especially a

streptococcal infection, and mastitis in particular (claimed). GapC

proteins are also used in claimed methods for detecting GapC antibodies,

and to raise antibodies that are used in claimed methods for detecting

GapC proteins. S. agalactiae is a common pathogen associated with

mastitis in cattle, horse, sheep and goat. It also causes septicemia,

meningitis, bacteraemia, impetigo, arthritis, urinary tract infections,

abcesses, spontaneous abortion, etc ., ,, 207 147 ๙ 87 54 Novel isolated GapC protein of Streptococcus dysgalactiae, S.agalactiae S.uberis, S.parauberis, or S.iniae, useful as vaccine component for treating streptococcal infection which causes mastitis in vertebrates. plasmin-binding protein; AgalGapC; infection; mastitis; vaccine; 88 KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEALEGTVEVKDGGFDVNGKFIKVSAE 28 MVVKVGINGFGRIGRLAFRRIONVEGVEVTRINDLTDPNMLAHLLKYDTTOGRFDGTVEV 148 KDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGQFVKVSAEREPANIDWATDGVEIVLE ----DGTVEVKEGGFEVNGQFVKVSAEREPANIDWATDGVEIVLE ATSFFAKKEAAEKHLHANGAKKVVITAPGGNDVKTVVFNTNHDILDGTETVISGASCTTN Gaps 85; Length 336; Indels gapC plasmin binding protein. Potter AA; Score 1557.5; DB 5; Pred. No. 8.1e-121; DB 5; Fontaine M, Claim 1(b); Fig 2A-B; 107pp; English. 15; 12-JUN-2000; 2000US-0211022P 11-JUN-2001; 2001WO-CA000838 68.4%; larity 73.9%; Conservative 1 , D (UYSA-) UNIV SASKATCHEWAN Streptococcus agalactiae Streptococcus agalactiae Perez-Casal WPI; 2002-130725/17. Similarity N-PSDB; ABA91249 Sequence 336 AA; WO200196381-A2. 20-DEC-2001. 311; Bolton AJ, 96 Н Query Match Best Local GapC; Matches XBX Б ò d d Dp à FX XX RX ਠੇ 8

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The invention relates to a protein comprising or having at least lost identified in the identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the streptococcus pneumoniae type 4 strain genomic sequence appearing as treptococcus patient by administering the protein, DNA or antibody (in a treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the composition), a kit comprising first and second primers, which are the sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence to sequence on tainer is substantially complementary to the target sequence the first primer is substantially complementary to the target sequence and where the parts of the primers having the target sequence to be amplified, assay comprising contactium, where one or more genes or encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus cut in an announced and preventing a such as pneumoniae, such as pneumoniae, such as pneumoniae, such as pneumoniae, such as pneumoniae, such as pneumoniae, such as pneumoniae, of the proteins of the proteins are such as pneumoniae, of the proteins of the proteins and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus
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useful as medicaments for treating or preventing a disease or infection
due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
antiinflammatory; antibacterial; immunostimulant; auditory; respiratory
KAIGLVIPELNGKLDGAAQRVPVPTGSVTELVATLEKDVTVEEVNAAMKAAANDSYGYTE
                                                                             YFAKIA
                                          DPIVSSDIVGVSYGSLFDATQTKVMEVDGSQLVKVVSWYDNEMSYTAQLVRTLE:
                                                               276 DPIVSSDIVGISYGSLFDATQTKVQTVDGNQLVKVVSWYDNEMSYTSQLVRTLE
                                                                                                                                                                                                                                                                                                                                                                                                    S. pneumoniae type 4 strain protein from coding region #2094.
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                                                                                                                                                                                                                                                                     standard; protein; 335 AA.
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N-PSDB; ABX07806.
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media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to standardise OS field)
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                                                                                                                                                      Length 335;
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Pred. No. 6e-119;
                                                                                                                                                                                    Mismatches
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23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The present sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in the printed pot sequences
                                                                                                                    Carr GJ;
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2000US-0253625P.
2000US-0257931P.
2001US-0269308P.
                                                                                                                    Ohlsen KL,
                                                                                 ELITRA PHARM INC
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N-PSDB; AAS55435.
 27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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Yamamoto RT,
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359 AA; Sequence

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                       Gaps
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                        86;
 Length 359;
                       Indels
ch 67.4%; Score 1535; DB 4; 1 Similarity 73.6%; Pred. No. 6.6e-119; 310; Conservative 12; Mismatches 13;
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                   Copyright
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- protein search, using sw model OM protein

March 29, 2004, 16:31:39; Search time 31.5224 Seconds (without alignments) 733.715 Million cell updates/sec Run on:

score: Title: Perfect

US-10-650-369-22 2278 1 MKKITGIILLLLAVIILSAC......EMSYTAQLVRTLEYFAKIAK Sequence:

448

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

51625971 residues 389414 segs, Searched: hits satisfying chosen parameters: 9 Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued_Patents_AA:*
'cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
'cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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'cgn2_6/ptodata/2/iaa/backfiles1.pep:* H Q W 4 N 0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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v	557.	80	3	4	-878-766A-	equence 14, App
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17	200	9	4	4	-09-134-000C-440	equence 4400, A
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ALIGNMENTS

	TYPE: PRT CRGANISM: Artificial Sequence CRGANISM: Artificial Sequence FEATURE: COTHER INFORMATION: Description of Artificial Sequence: GapC multiple COTHER INFORMATION: epitope fusion protein US-09-878-766A-22	Query Match Best Local Similarity 100.0%; Pred. No. 1.7e-206; Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 MKKITGIILLLAVIILSACQANYGSGMVVKVGINGFGRIGRLAFRRIQNVEGVEVTRIN 60 	Oy 61 DLTDPNMLAHLLKYDTTQGRFDGTVEVKEGGFEVNGNFIKVSAERDPENIDWATDGVEIV 120 	Qy 121 LEALEGTVEVKOGGFDVNGKFIKVSAEKDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVN 180 	Oy 181 GQFVKVSAEREPANIDWATDGVEIVLEATSFFAKKEAAEKHLHANGAKKVVITAPGGNDV 240 	Oy 241 KTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHAYTGDQMIL 300 	Oy 301 DGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRVPVPTGSVTELVV 360

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                                                                                                                                                                                            APPLICANT: Potter, Andrew A.
APPLICANT: Potter, Andrew A.
APPLICANT: Potter, Andrew A.
APPLICANT: Pottaine, Michael
TITLE OF INVENTION: MMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 336
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Pred. No. 5e-148;
0; Mismatches
                                                                        ; ORGANISM: Streptococcus dysgalactiae
US-09-878-766A-12
                                                                                                                                                            Sequence 12, Application US/09878766A Patent No. 6660270 GENERAL INFORMATION:
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US-07-928-462-2
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         APPLICANT: Boyle, Michael D.P.
APPLICANT: Lottenberg, Richard
APPLICANT: Lottenberg, Richard
APPLICANT: Broder, Christopher C.
APPLICANT: von Mering, Gregory O.
TITLE OF INVENTION: Bacterial Plasmin Receptors as
TITLE OF INVENTION: Fibrinolytic Agents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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Pred. No. 1.2e-147;
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REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-13.C2
SLECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 32606
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,462
FILING DATE: 19920810
CLASSIFICATION: 424
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APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411
FILING DATE: 16-MAY-1990
PRIOR APPLICATION DATA:
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larity 79.1%;
Conservative
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FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
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GENERAL INFORMATION:
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Sequence 16, Application US/09878766A

Sequence 16, Application US/09878766A

Patent No. 6660270

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Perez-Casal, Jose

APPLICANT: Potter, Michael

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16

LENGTH: 336

TYPE: PRT
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US-09-878-766A-16
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nes 311; Conser
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28 MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEV
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                                                                                                                                                         US-08-2,
Sequence 2, Apr-
Sequence 2, Apr-
Sequence 2, Apr-
Patent No. 6136323
GENERAL INFORMATION:
APPLICANT: Boyle, Michael D.P.
APPLICANT: Lottenberg, Richard
APPLICANT: Lottenberg, Richard
APPLICANT: Von Mering, Gregory O.
TITLE OF INVENTION: Fibrinolytic Agents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
FL
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,247
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/524,411
FILING DATE: 16-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,849
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-13.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-372-5800
TELEFAX: 904-372-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1652.5; DB 3, Pred. No. 1.2e-147; 2; Mismatches 1;
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1 Similarity 79.1%;
333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 336 amino aci
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US-08-273-247-2
                                                                 K 448
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US-08-273-247-2
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Pred. No. 1.1e-1
5; Mismatches
                                                                                                        Sequence 14, Application US/09878766A

Batent No. 6660270

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Perez-Casal, Jose

APPLICANT: Fontaine, Michael

TITLE OF INVENTION: MACHINET STREPTOCOCCUS INI

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INI

FILE REFERENCE: 9000-0057

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-878-766A-20
; Sequence 20, Application US/09878766A
; Patent No. 6660270
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
                                                                                                                                                                                                                                                                                                          Streptococcus agalactiae
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Best Local Similarity 73.9%;
Matches 311; Conservative 15
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ION: AGAINST STREPTOCOCCUS INFECTION
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FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.6e-136;
7; Mismatches 13;
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US-09-878-766A-18

Sequence 18, Application US/09878766A

Batent No. 6660270

GENERAL INFORMATION:

APPLICANT: Porter, Andrew A.

APPLICANT: Perez-Casal, Jose

APPLICANT: Fontaine, Michael

TITLE OF INVENTION: IMMUNIZATION OF DAIRY CA

TITLE OF INVENTION: AGAINST STREPTOCOCCUS I

FILE REFERENCE: 9000-0057
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Pred. No.
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nilarity 72.7%;
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LENGTH: 336
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LENGTH: 336
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Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vacci
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                          1 MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDFNMLAHLLKYDTTQGRFU
                                                                                                                                            148 KDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGQFVKVSAEREPANIDWATDGV
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8
Indels
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ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: 1707
Mismatches
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
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R: PB340P2
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (301) 309-8512
NFORMATION FOR SEQ ID NO: 54
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino in it.
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 Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIGLVIPELNGKLDGAAQRVPVPTGSVTELVVTLDKNVSVDEINAAMKAASNDSFGYTED
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                                                                                                                                                                                                                  86;
                                                                                                                                                        Length 333;
                                                                                                                                                                                                                    Indels
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                                                                                                                                                      Score 1491; DB 3;
Pred. No. 2.1e-132;
2; Mismatches 17;
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION SATA:
APPLICATION NUMBER: 08/96'
FILING DATE: OCT-26
ATTORNEY/AGENT TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inc.
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FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
ORMATION FOR SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDARY SECONDA
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STREET: 9410 Key West Avenue
CITY: Rockville
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                                                                                                                                                          Query Match
Best Local Similarity 72.4%;
Matches 302; Conservative
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COUNTRY: USA
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-54
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                                                                                                                                                                                                29 VVKVGINGFGRIGRLAFRRIONVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFI
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Pred. No. 1.2e-11
5; Mismatches 4
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| Similarity 72.4%; Pred. No. 2
| 302; Conservative 12; Mismatche
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AN
                                                                                         ID NO:
          LENGTH: 333 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID N
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llarity 62.5%;
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CHARACTERISTICS
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Best Local Similarity
Matches 262; Conser
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US-09-536-784-54
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Best Local S
Matches 302
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SSULT 12
5-09-107-532A-4769
Sequence 4769, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                 267
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98
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                                                                                                                 228 KAIGLVIPELNGKLDGAAQRVPVATGSLTELVTVLDKEVTVDEVNAVMEKAANESYGYNT
                                148 KDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGQFVKVSAEREPANIDWATDGVEIVLE
                                                                                                 ATSFFAKKEAAEKHLHANGAKKVVITAPGGNDVKTVVFNTNHDILDGTETVISGASCTTN
                                                                                                                                                                 CLAPMAKALHDAFG10KGLMTTIHAYTGDOMILDGPHRGGDLRRARAGAANIVPNSTGAA
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5007
                                                                     --GEL-
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LOCATION: (B) LOCATION 1...333
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SEQUENCE DESCRIPTION: SEQ ID NO: 4769
US-09-107-532A-4769
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COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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Waltham: Massachusetts
   74 HEGSFNVNGKEIKVLANRNPEELPW
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LENGTH: 333 amino acide
TYPE: amino acid
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TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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ADDRESSEE: GENOME
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CITY: Wa
STATE: M
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Sequence 4229, Application US/09134000C
Sequence 4229, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BNTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4229
LENGTH: 357
CTGFYTDKEKAQAHIDA-GAKKVLISAPAKGDVKTIVFNTNHDTLDGSETVVSGASCTTN
                                                                                                                                                                     KAIGLVIPELNGKLDGAAQRVPVPTGSVTELVVTLDK-NVSVDEINAAMKAASNDSFGYT
                                               CLAPMAKALHDAFGIQKGLMTTIHAYTGDQMILDGPHRGGDLRRARAGAANIVPNSTGAA
                                                                28 MVVKVGINGFGRIGRLAFRRIQNV-EGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVE
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Sequence 5513, Application US/09134001C

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO E

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
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             ch 55.8%; Score 1270; DB 4 11 Similarity 62.1%; Pred. No. 1.5e-11 260; Conservative 26; Mismatches 4
                                                                                                                                                                     61 HEGSFNVNGKEVKVLANRNPEELPW---
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EQ ID NO 5513
LENGTH: 348
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US-09-134-001C-5513
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ORGANISM:
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275 PSFGWNEDEIVSSDVIGTTYGSIFDPTQTEVTTAGDYQLVKTVAWYDNEYGFTCQMIRTL 334
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1 MTVKIGINGFGRIGRLAFRRIYEIGAKSNDIQVVAINDLTSPTMLAHLLKYDSTHGTFFG 60
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                                                             GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, Ilkka J.

APPLICANT: Havukkala, Ilkka J.

APPLICANT: Lubbers, Mark W.

APPLICANT: Lubbers, Mark W.

APPLICANT: Christensson, Anna C.

APPLICANT: Christensson, Anna C.

APPLICANT: O'Toole, Paul W.

APPLICANT: O'Toole, Paul W.

APPLICANT: Reid, Julian R.

APPLICANT: Coolbear, Timothy

TITLE OF INVENTION: Polynucleotides, materials incorporating

TITLE OF INVENTION: them and methods for using them.

FILE REFERENCE: 11000.1043U1

CURRENT APPLICATION NUMBER: US/09/634,238

CURRENT FILING DATE: 2000-08-08

NUMBER OF SEQ ID NOS: 422

SOFTWARE: FastSEQ for Windows Version 4.0

SEC IN NO 23-2
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                                     233, Application US/0963423
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RESULT 15
US-09-634-238-233
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Search time 73.5522 Seconds (without alignments) 1593.758 Million cell updates/sec •• 2004, 16:35:22 29, March Run on:

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hits satisfying chosen parameters of Total number

length: 0 length: 2000000000 នeq នeq 0B 0B Maximum Minimum

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45 summaries Published

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Published Applications AA:*

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| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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SUMMARIES

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9	165	ζ.	M		-878-781-1	equence 14, App
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Φ	559,	ω	ጥ	δ	39-878-766A-1	quence 16, Appl
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	557.	ω.	3	10	9-878-781-	Sequence 6. Appl
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	53	7.	S	σı	US-09-815-242-13169	quence 13169, A
	53	7.	359	12	US-10-282-122A-74186	e 74186,

quence 20, Apequence 12, Aequence 12, Aequence 12, Aquence 13593,	Sequence 18, App Sequence 10, Ap Sequence 72254, Sequence 54, App Sequence 18524, equence 10847, Sequence 57294,	Sequence 53266, Sequence 53266, Sequence 51519, Sequence 71734, Sequence 65661, Sequence 65001, Sequence 65001,	26 5618 30 1254 30 1254 30 1254 30 1254 30 1254 30 1255 30 1255 30 1255 30 1255 30 1255 30 1255 30 1255 30 1255
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Sequence 22, Application US/09878766A
Sequence 22, Application US/09878766A
Sequence 22, Application US/09881
GENERAL INFORMATION:
APPLICANT: Perez-Casal, Jose
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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RESULT 1
US-09-878-766A-22
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LENGTH: 448
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Score 1656.5; DB 1
Pred. No. 1.2e-142;
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; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus dysgalactiae
US-09-878-781-4
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Publication No. US20030165524A1
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
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nilarity 79.6%;
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; Sequence 12, Application US/09878766A
; Patent No. US20020044928A1
; GENERAL INFORMATION:
    APPLICANT: Potter, Andrew A.
    APPLICANT: Potter, Andrew A.
    APPLICANT: Potter, Michael
    TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHI
    TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
    FILE REFERENCE: 9000-0057
; CURRENT APPLICATION NUMBER: US/09/878,766A
; CURRENT FILING DATE: 2001-09-10
    NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 336
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Sequence 4, Application US/09878181
Sequence 4, Application US/09878181
Sequence 4, Application US20030082781A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Perca Casal, Jose
APPLICANT: Perca Casal, Jose
APPLICANT: Porter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055
CURRENT APPLICATION NUMBER: US/09/878,781
CURRENT FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Identification of Essential
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTL
TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055.20
CURRENT APPLICATION NUMBER: US/10/134,297
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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; Sequence 74379, Application US/10282122A
; Publication No. US20040029129A1
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robe
Ohlsen, Kari
Zyskind, Judith
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Pred. No. 1.5e-142;
.; Mismatches 1;
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PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 74379
LENGTH: 336
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Streptococcus pyogenes US-10-282-122A-74379
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APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
APPLICANT: Fontaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055
CURRENT APPLICATION NUMBER: US/09/878,781
CURRENT FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 335
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Pred. No. 4.9e-142;
; Mismatches 0;
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; Publication No. US20030082781A1
; Publication No. US20030082781A1
; GENERAL INFORMATION:
; APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
; APPLICANT: Portaine, Michael
APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CA'
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0055
; CURRENT FILING DATE: 2002-09-10
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
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llarity 79.1%;
Conservative
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Best Local Similarity
Matches 333; Conser
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GENERAL INFORMATION:
APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
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                                                   Artificial
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CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 336
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                                                  ; OTHER INFORMATION: Description
; OTHER INFORMATION: protein
US-09-878-781-16
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nilarity 73.9%;
Conservative 15
           TYPE: PRT
ORGANISM: Artificial Sequence
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76.2%;
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Patent No. US20020044928Al
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; TYPE: PRT
; ORGANISM: Streptococcus uberis
US-10-134-297-8
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Best Local Similarity 73.9%; Pred. No. 9e-134;
Matches 311; Conservative 15; Mismatches 1
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Publication No. US20030082781A1;
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose;
APPLICANT: Portaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTI
TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055
CURRENT APPLICATION NUMBER: US/09/878,781
CURRENT FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIN Ver. 2.0
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Sequence 8, Application US/10134297
Publication No. US20030165524A1
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055.20
CURRENT APPLICATION NUMBER: US/10/134,297
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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                                                                            APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
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; Publication No. US20030082781A1
; GENERAL INFORMATION:
; APPLICANT: Bolton, Alexandra J.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; APPLICANT: Fotter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTL;
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0055
; CURRENT APPLICATION NUMBER: US/09/878,781
                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
EQ ID NO 14
LENGTH: 336
                US/09878766A
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  patence 14, Application US/
Patent No. US20020044928A1
GENERAL INFORMATION:
APPLICANT: Perez-Casal, Trapplicant: Perez-Casal, Trapplicant: Perez-Casal, Trapplicant.
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Sequence 6, Application US/10134297
Sublication No. US20030165524A1
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055.20
CURRENT APPLICATION NUMBER: US/10/134,297
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                      ch (8.4%; Score 1557.5; DB 10 (1 Similarity 73.9%; Pred. No. 1.4e-133; 311; Conservative 15; Mismatches 10;
                                                                                                  ; ORGANISM: Streptococcus agalactiae
US-09-878-781-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus agalactiae
CURRENT FILING DATE: 2002-09-10 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 336
TYPE: PRT
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                         Gaps
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ed. No. 1.7e-131;
Mismatches 13;
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    Pred.
 .larity 73.6%; Pr
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Matches 310; Conser
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Patent No. US2000505563A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
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APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Su. H. Howard

ITILE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: 60/191, 078

PRIOR PILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/207, 727

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-24

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

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PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

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                                                                                                                                                 Length 359;
                                                or
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                                                                                                                                                Query Match
Best Local Similarity 73.6%; Pred. No. 1.7e-131;
Matches 310; Conservative 12; Mismatches 13;
                                                See
PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed:
NUMBER OF SEQ ID NOS: 78614

SOFTWARE: Patentin version 3.1

LENGTH: 359
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                                                                                                                 , ORGANISM: Streptococcus pneumoniae US-10-282-122A-74186
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Job time : 100.552 secs
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version 5.1.6
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OM protein - protein search, using sw model

March 29, 2004, 16:26:39; Search time 26.7463 Seconds (without alignments) 1611.208 Million cell updates/sec Run on:

US-10-650-369-22 2278 1 MKKITGIILLLLAVIILSAC......EMSYTAQLVRTLEYFAKIAK

Title: Perfect score: Sequence:

448

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

	RESULT 1	
	A42963 glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) N:Alternate names: plasmin receptor	orylating) (EC 1.2.1.12) - Streptococcus
	C;Species: Streptococcus sp. C:Date: 10-Mar-1994 #sequence revision 10-Mar-199	34 #text change 03-Jun-2002
	C; Accession: A42963; B42963; JH0750	
	J. Bacteriol. 174, 5204-5210, 1992	i, 3.U.; SciilOedel, B.L.; Calciss iii, R
	A; Title: Cloning, sequence analysis, and expressi A; Reference number: A42963; MUID:92355491; PMID:1	on in Escherichia coli of a streptococc. 322883
	A; Accession: A42963 A: Molecule type: DNA	
	A;Residues: 1-336 <lot></lot>	
	A;Experimental source: group A, strain 64/14 A:Note: sequence extracted from NCBI backbone (NC	BIP:110308)
	A; Accession: B42963	
	A; Molecule Lype: procein A; Residues: 2-74;161-164,'X',166-174;187-211,'X',	213-217 <lo2></lo2>
	R; Pancholi, V.; Fischetti, V.A.	
). Exp. Med. 1/0, 413-420, 1992 A:Title: A major surface protein on group A strep	tococci is a glyceraldehyde-3-phosphate
	A; Reference number: JH0750; MUID: 92364544; PMID:1	500854
	A;Accession: JH0750 A;Molecule type: protein	
	A;Regidues: 2-30,'A',32-40 <pan></pan>	
-	C;Superiaminy: gryceraldemyde-3-phosphace demydrogemase C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; oxidoreductase F:152/Active site: Cvs #status predicted	genase amer; NAD; oxidoreductase
	Onerv Match 72.5%: Score 1652.5;	DB 2: Length 336:
	Best Local Similarity 79.1%; Pred. No. 9.1e-101; Matches 333; Conservative 2: Mismatches 1:	Tudela
		C
	Qy 28 MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEV	TDPNMLAHLLKYDTTQGRFDGTVEV 87
	Db 1 MVVKVGINGFGRIGRLAFRRIQNIEGVEVTRINDL	rbenmiahilkybriogreporvev 60
	QY 88 KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEALEGTVEVKDGGFDVNGKFIKVSAE	ALEGIVEVKDGGFDVNGKFIKVSAE 147
_	Db 61 KEGGFEVNGNFIKVSAERDPE	8
	Qy 148 KDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGQ	FVKVSAEREPANIDWATDGVEIVLE 207
	Db 82NIDWATDGVEIVLE	NIDWATDGVEIVLE 95
	Qy 208 ATSFFAKKEAAEKHLHANGAKKVVITAPGGNDVKT	WFNTNHDILDGTETVISGASCTIN 267
	Db 96 ATGFFAKKEAAEKHLHANGAKKVVITAPGGNDVKT	GAKKVVITAPGGNDVKTVVFNTNHDILDGTETVISGASCTTN 155
	Qy 268 CLAPMAKALHDAFGIQKGLMTTIHAYTGDQMILDGPHRGGDLRRARAGAANIVPNSTGAA 327	PHRGGDLRRARAGAANIVPNSTGAA 327

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glyceraldehyde 3-phosphate dehydrogenase [imported] - Streptococcus pneumoniae (strain 1 c) Species: Streptococcus pneumoniae () Species: Streptococcus pneumoniae () Species: Streptococcus pneumoniae () Species: Streptococcus pneumoniae () Species: Streptococcus pneumoniae () Species: O1-Aug-2001 () Streptococcus pneumoniae () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus pneumoniae () Streptococcus pneumoniae () Streptococcus pneumoniae () Streptococcus pneumoniae () Streptococcus pneumoniae () Streptococcus () Streptococcus pneumoniae () Streptococcus () Streptococcus pneumoniae () Streptococcus () Streptococcus pneumoniae () Streptococcus () Streptococcus pneumoniae () Streptococcus () Streptococcus pneumoniae () Streptococcus () Streptococcus pneumoniae () Streptococcus () Streptococcus pneumoniae () Streptococcus () Streptococcus pneumoniae () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococcus () Streptococ
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C;Species: Streptococcus "equisimilis"
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2
C;Accession: S71350
C;Accession: S71350
C;Accession: S71350
A;Title: Cloning, sequencing and functional overexpression of the Strept inding protein. Purification and biochemical characterization of the pro A;Reference number: S71350; MUID:96305364; PMID:8706717
A;Residues: 1-336 <GAS>
A;Residues: 1-336 <GAS>
A;Residues: 1-336 <GAS>
A;Cross-references: EMBL:X97788; NID:gl478268; PIDN:CAA66377.1; PID:gl47
A;Experimental source: strain H46A
C;Genetics:
A;Gene: gapC
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; NAD; oxidoreductase
C;Keywords: gluconeogenesis; glycolysis; NAD; oxidoreductase
C;Keywords: gluconeogenesis; glycolysis; NAD; brinding fold
F;152/Active site: Cys #status predicted
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Pred. No. 1.3e-94;
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                              Gaps
                             86;
Length 335;
                             Indels
                  93;
13;
  Score 1535; DB 2;
Pred. No. 4.4e-93;
2; Mismatches 13;
                            12;
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 Query Match
Best Local Similarity 73.6%;
Matches 310; Conservative 1
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hypothetical protein gapA [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C; Species: Lactococcus lactis subsp. lactis (Species: Lactococcus lactis subsp. lactis (Species: Lactococcus lactis subsp. lactis (Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C; Accession: G86694
R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001
A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Residues: DNA
A; Residues: 1-337 <STO>
A; Residues: 1-337 <STO>
A; Residues: 1-337 <STO>
A; Experimental source: strain IL1403
            28 MVVKVGINGFGRIGRLAFRRIONVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEV 87
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A;Gene: gapA
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
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A; Title: Genome of the Bacterium Streptococcus pneumoniae S
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: G98099
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-359 < KUR>
A; Cross-references: GB:AE007317; PIDN:AAL00628.1; PID:g1545
C; Genetics:
A; Gene: gapA
C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C; Keywords: oxidoreductase
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Superfamily: glyceraldehyde-3-phosphate dehydrogenase
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.; C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Teference number: ABIO77; MUID:21537279; PMID:11679669
A;Accession: AC1382
A;Status: preliminary
A;Molecule type: DNA
A;References: GB:NC_003210; PIDN:CAD00537.1; PID:gl6411947; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: gap
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
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              CLAPMAKALHDAFGIQKGLMTTIHAYTGDQMILDGPHRGGDLRRARAGAANIVPNSTGAA
                             SLAPMADALNKNFGVKGGTMTTVHSYTGDQMTLDGPHRGGDFRRARAAAENIVPASSGAA
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C;Species: Clostridium pasteurianum
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-Jun-2
C;Accession: S34254
R;Oster, T.; Assobhei, O.; Scherrer, S.; Branlant, G.; Branlant, C.
submitted to the EMBL Data Library, May 1993
A;Description: Nucleotide sequence of the glyceraldehyde-3-phosphate deh
A;Reference number: S34254
A;Accession: S34254
A;Molecule type: DNA
A;Residues: 1-334 <OST>
A;Coss-references: EMBL:X72219; NID:g311923; PIDN:CAA51020.1; PID:g3119
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: oxidoreductase
                                                                       KAIGLVIPELNGKLDGAAQRVPVPTGSVTELVVTLDKNVSVDEINAAMKAASND
                                                                                     TSFFAKKEAAEKHLHANGAKKVVITAPGGNDVKTVVFNTNHDILDGTETVISG
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larity 59.3%; Pred. No. 2.1e-73;
Conservative 34; Mismatches 51;
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                                                                                         88 KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEALEGTVEVKDGGFDVNGKFIKVSAE
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                                                                                                                                                                                               96 CTGFFTAQDKAELHIKA-GAKKVVISAPATGDMKTIVYNVNHETLDGTETVISGASCTTN
                                                                                                                                                                                                                                                                                      275 SDQVVSSDIKGMTFGSLFDETQTKVLTVGDQQLVKTVAWYDNEMSYTAQLVRTLEYFAKI
                                                         148 KDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGQFVKVSAEREPANIDWATDGVEIVLE
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                      87;
 Length
                       Indels
 Score 1205.5; DB 2;
Pred. No. 1.5e-71;
1; Mismatches 54;
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1 Similarity 58.5%;
247; Conservative 3
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steria monocytogenes

gap [imported]

glyceraldehyde 3-phosphate dehydrogenase homolog gap [imported] - Listeria C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AC1382

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glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) C NWA0246 [impoc 5: Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Species: O5-May-2000 #text_change 03-Jun-2002
C; Date: O5-May-2000 #text_change 03-Jun-2002
C; Date: O5-May-2000 #text_change 03-Jun-2002
C; Date: O5-May-2000 #text_change 03-Jun-2002
C; Date: O5-May-2000 #text_change 03-Jun-2002
C; Date: O5-May-2002
C; Mature 404, 502-506
C; Leather, S.; Moule, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A; Reference number: A81775; MUD:2022556; PMID:10761919
A; Reference number: A81775; MUD:2022556; PMID:10761919
A; Residues: DNA
A; Residues: DNA
A; Residues: DNA
A; Residues: GB:AL162752; GB:AL157959; NID:g737878; PIDN:CAB83554.1; PID:g73790C
C; Genetics:
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61;
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                                61 EGAFVVNGKEVKVFAEADPEKLPWG
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Best Local Similarity
Matches 235; Conser
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                                                                                                                                                 Score 1204.5; DB 2;
Pred. No. 1.8e-71;
33; Mismatches 55;
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A;Cross-references: GB:AL592022; PIDN:CAC97780.1; A;Experimental source: strain Clip11262 C;Genetics: A;Gene: gap C;Superfamily: glyceraldehyde-3-phosphate dehydrog
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E81001
glyceraldehyde 3-phosphate dehydrogenase NMB2159 [imported] - Neisseria meningitidis
c;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: E81001
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R;Tettelin, H.; Saunders, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
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ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V. A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUID:20175755; PMID:10710307
A; Accession: E81001
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-334 < TET>
A; Residues: 1-334 < TET>
A; Residues: 1-334 < TET>
A; Cross-references: GB: AE002563; GB: AE002098; NID:g7227405; PIDN: AAF42467.1; PID:g72274:
A; Experimental source: serogroup B, strain MC58
C; Genetics:
A; Genetics:
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A; Genetics:
C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase
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A; Accession: T09633
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-338 <BRA>
A; Residues: 1-338 <BRA>
A; Residues: 1-338 <BRA>
A; Cross-references: EMBL:AJ000339; NID:92624189; PIDN:CAA04014.1; PID:92624191
A; Experimental source: subsp. bulgaricus, strain B107
C; Genetics:
A; Gene: gap
C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C; Keywords: gluconeogenesis; glycolysis; oxidoreductase
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Matches 232; Conservative 37; Mismatches 62;
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R; Branny, P.; Delatorre, F.; Garel, J.R.
Microbiology 144, 905-914, 1998
A; Title: An operon coding for three glycolytic enzy
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MLAHLLKYDTTQGRFDG 83	Escherichia coli (strain O157:H7_change 03-Aug-2001_hii, K.; Yokoyama, K.; Han, C.G.ri, M.; Shinagawa, H. scherichia coli O157:H7 and genc_scherichia coli O157:H7 and genc_3361488; GSPDB:GN00154_09952	5; DB 2; Length 333; 2.7e-54; hes 76; Indels 91; Gaps 7; NDLTDPNMLAHLLKYDTTQGRFDGTVEVKE 89 NDLTSPKILAYLLKHDSNYGPF 54 VLEALEGTVEVKDGGFDVNGKFIKVSAEKD 149
28 MYVKVGINGFGRIGRLAFRRIONVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDG 1 MTVKIGINGFGRIGRLAFRRIMDLGBETKDIEVVAINDLTTPAMLAHLLKYDTTQGRFDH 84 TVEVKEGGFEVNGNPIKVSAERDPENIDMATDGVEIVLEALEGTVEVUGGFDVNGKFIK 61 EVSATEDSLVVDGKKYRVYAEPQAQNIPMVKN 144 VSAEKDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGGFVKVSAEREPANIDMATDGVE 93	phosphate dehydrogenase C [imported] - ichia coli 01 #sequence_revision 18-Jul-2001 #text 81 kino, K.; Ohnishi, M.; Kurokawa, K.; Is unaga, T.; Kuhara, S.; Shiba, T.; Hatto 2001 genome sequence of enterohemorrhagic E r: A99629; MUID:21156231; PMID:11258796 81 cary bNA <hay> s: GB:BA000007; PIDN:BAB35445.1; PID:g1 urce: strain 0157:H7, substrain RIMD 05</hay>	### ##################################
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Search completed: March 29, 2004, 16:35:57 Job time : 28.7463 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 29, 2004, 15:59:33; Search time 19.1045 Seconds (without alignments) 1221.045 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

448 US-10-650-369-22 2278 1 MKKITGIILLLLAVIILSAC......EMSYTAQLVRTLEYFAKIAK

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

(GAPDH)

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collaboration -
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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F06006EE253C8A3F CRC64;
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EMBL; AE006494; AAK33348.1; -.
EMBL; AE009973; AAL97041.1; -.
HSSP; P00362; 1GD1.
InterPro; IPR000173; GAP_dhdrogenase.
InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD; Complete proteome.
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Pred. No. 1.2e-93;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=SSI-1 / Serotype M3;

K Madellossin N.A.

STRAIN=SSI-1 / Serotype M3;

Macagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,

Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,

Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,

Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,

Hayashi H., Hattori M., Hamada S.;

"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a large-scale genomic rearrangement in invasive strains and new insight into phage evolution.";

Genome Res. 13:1042-1055(2003).

-!- FUNCTION: ALSO BINDS HUMAN PLASMINOGEN (By similarity).

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + Phosphate

NAD(+) = 3-phospho-D-glycerolylsis; first step.

-!- PATHWAY: Second phase of glycolysis; first step.

-!- SUBUNIT: Homotetramer (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
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                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYCERALDEHYDE 3-PHOSPHATE (BY SIMILARITY).
ACTIVATES THIOL GROUP DURING CA
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (C Plasminogen-binding protein) (Plasmin receptor).
GAP OR PLR OR SPYM3 0201 OR SPS0207.
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                         emergence.";
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
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Pred. No. 2.1e-93;
1; Mismatches 2;
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EMBL; AP005141; BAC63302.1; -.
InterPro; IPR000173; GAP_dhdrogenase.
InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
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TIGRFAMS; TIGR01534; GAPDH-1; 1.
PROSITE; PS00071; GAPDH; 1.
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NCBI_TaxID=198466;
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G3P_STRP3 ID G3P_STRP3 AC Q8K8M9;

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VVKVGINGFGRIGRLAFRRIQNIEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEVK
                                                                                     DPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGQFVKVSAEREPANIDWATDGVEIVLEA
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MEDLINE=96305364; PubMed=8706717;

Gase K., Gase A., Schirmer H., Malke H.;

"Cloning, sequencing and functional overexpression of the streptococcus equisimilis H46A gapC gene encoding a glyceraldehyde-3-phosphate dehydrogenase that also functions as plasmin(ogen)-binding protein. Purification and biochemical characterization of the protein.";

Eur. J. Biochem. 239:42-51(1996).

-!- FUNCTION: ALSO BINDS HUMAN PLASMINOGEN.

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate NAD(+) = 3-phospho-D-glyceraldehyde 3-phosphate + NADH.

-!- SUBGELLULAR LOCATION: Cytoplasmic.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
                          EGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEALEGTVEVKDGGFDVNGKFI
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)
(Plasminogen-binding protein) (Plasmin receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus equisimilis.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae
Streptococcus.
                                                EMBL; X97788; CAA66377.1;
EMBL; Y12602; CAA73174.1;
PIR; S71350; S71350.
HSSP; P00362; 1GD1.
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SEQUENCE FROM
STRAIN=H46A;
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G3P_STREQ
TD G3P_STREQ
Q59906;
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FE7ACFDFD7663E46 CRC64;
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STRAIN=LM0230;
MEDLINE=95291425; PubMed=7773380;
Cancilla M.R., Hillier A.J., Davidson B.E.;
"Lactococcus lactis glyceraldehyde-3-phosphate dehydrogenase gene, gap: further evidence for strongly biased codon usage in glycolytic
                                                                                                                                                                                                                                     85;
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                                                                                                                            3-PHOSPHATE
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                                                                                                                                                                                                          Score 1553.5; DB 1;
Pred. No. 9.5e-88;
; Mismatches 14;
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                                                                                                                         GLYCERALDEHYDE
SIMILARITY).
                                                                                                               BY SIMILARITY
     enase
InterPro; IPR000173; GAP_dhdrogena InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD.
INIT_MET 0 0 8Y SI
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STRAIN=IL1403;
MEDLINE=21235186; PubMed=11337471;
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Microbiology 141:1027-1036(1995)
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                                                                                                                                                                                   35739 MW;
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76.0%;
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Best Local Similarity 76.0
Matches 319; Conservative
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Bacteria; Firmicutes;
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lilactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosply NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
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EMBL; AE006290; AAK04657.1; -.
EMBL; AE006290; AAK04657.1; -.
PIR; G86694; G86694.
HSSP; P17721; 1HDG.
InterPro; IPR000173; GAP dhdrogenase.
InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh; 1.
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Pfam; PF028000; gpdh; 1.
Pfam; PF028000; gp
             O., Malarme K.,
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46;
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Pred. No. 4.2e-71
1; Mismatches 4
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ACTIVATES THIOL
(BY SIMILARITY).
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larity 61.4%;
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337 AA;
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MEDLINE=98291870; PubMed=9629918;

REDLINE=98291870; PubMed=9629918;

Reduence analysis of proteins from Clostridium pasteurianum W5.";

Electrophoresis 19:802-806(1998).

C -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NADH.

C -!- PATHWAY: Second phase of glycolysis; first step.

C -!- PATHWAY: Second phase of glycolysis; first step.

C -!- SUBUNIT: Homotetramer (By similarity).

C -!- SUBCELLULAR LOCATION: Cytoplasmic.

C -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate

dehydrogenase family.
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ACTIVATES THIOL GROUP DURING CATALYSIS
D15905D0DA7F62E7 CRC64;
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                                                                                                                                                                                                                       (GAPDH)
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                                                                                                                                                                                                                                                                                                                                                                                                       Oster T., Assobhei O., Scherrer S., Branlant G., Branlant Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)
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larity 59.3%; Pred. No. 2.6e-68;
Conservative 34; Mismatches 51;
                                                                                                                                                                                                                                                                           Clostridium pasteurianum.
Bacteria; Firmicutes; Clostridia; Clostridiales;
Clostridium.
NCBI_TaxID=1501;
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PIR; S34254; S34254.
HSSP; P00362; 1GD1.
InterPro; IPR000173; GAP_dhdrogenase.
InterPro; IPR006424; GAPDH-I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD.
BINDING 150 150 GLYCE
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249; Conser
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Matches 249
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
GAP OR GAPC OR CAC0709.
Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schreiber W., Durre P.;
"The glyceraldehyde-3-phosphate dehydrogenase of Clostridium acetobutylicum: isolation and purification of the enzyme, and sequencing and localization of the gap gene within a cluster of glycolytic genes.";
Microbiology 145:1839-1847(1999).
                                                                                                                                                           LAPMAKVLNDKFGIEKGFMTTIHAYTNDQNTLDGPHRKGDFRRARAAVSIIPN
                                                                                                                                                                                                                                                                 STRAINE FROM N.A.

STRAINE ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE=21359325; PubMed=11466286;

MEDLINE=21359325; PubMed=11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q. Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-product bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate NADH.

-!- PATHWAY: Second phase of glycolysis; first step.

-!- SUBUNIT: Homotetramer.

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
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                                  -GEL-
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                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                              VAD; Complete proteome.
GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING CATALYSIS
1 10C52A174BE789B5 CRC64;
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STRAIN=ATCC 12228;

PubMed=12950922;

Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

Qin Z.-Q., Miao Y.-G., wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

Qin Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;

"Genome-based analysis of virulence genes in a non-biofilm-forming staphylococcus epidermidis strain (ATCC 12228).";

Mol. Microbiol. 49:1577-1593 (2003).

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NADH.

NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.

-!- PATHWAY: Second phase of glycolysis; first step.
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Q8CPY5;
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 43, Last annotation update)
17-MAR-2004 (Rel. 43, Last annotation update)
18-MAR-2004 (Rel. 43, Last annotation update)
18-MAR-2004 (Rel. 43, Last sequence update)
18-MAR-2004 (Rel. 43, Last sequence update)
18-MAR-2004 (Rel. 43, Last sequence update)
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18-MAR-2004 (Rel. 43, Last sequence update)
18-MAR-2004 (Rel. 43, Last sequence update)
18-MAR-2004 (Rel. 43, Last sequence update)
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18-MAR-2004 (Rel. 43, Last sequence 
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Pred. No. 2e-66;
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PIR; C96987; C96987.

HSSP; P17721; 1HDG.
InterPro; IPR000173; GAP dhdrogena:
InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMB; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH-I; 1.
Glycolysis; Oxidoreductase; NAD; CcBINDING 150 GLYCER
ACT SITE 177 177 ACTIVESEQUENCE 334 AA; 35850 MW; 10CE
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                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GLYCERALDEHYDE 3-PHOSPHATE (B
SIMILARITY).
ACTIVATES THIOL GROUP DURING
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                               Length
plasmic (By similarity).
glyceraldehyde 3-phosphate
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Pred. No. 1.7e-62;
); Mismatches 61;
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G3P1 STAAM
G3P1 STAAM
STANDARD; PRT; 336 AA.
Q9Z5C5;
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase 1 (ECGAPA OR GAP OR SAV0772 OR SA0727 OR MW0734.
  Cytoplasmic the glycera
                                                                                                                                                                   InterPro; IPR006424; GAPDH-I.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh_C; 1.
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PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD BINDING 151
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ilarity 55.7%;
Conservative 3
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SUBCELLULAR LOCATION: C SIMILARITY: Belongs to dehydrogenase family.
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235; Conser
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                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN=Muso / ATCC 700699, and N315;

MEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

A Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

A Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

A Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

A Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

A Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus

I aureus.";
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SEQUENCE FROM N.A.
STRAIN=MW2;
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Magai Y., Twama N., Asano K., Naimi T., Kuroda H., Cui L.,
Nagai Y., Hiramatsu K.;
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
"Genome and virulence determinants of high virulence community-
"Genome and virulence determinants of high virulence community-
"Genome and virulence determinants of high virulence community-
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Morrissey J.A., Williams P.;
"Isolation and characterisation of a glycolytic operon in
Staphylococcus aureus.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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GLYCERALDEHYDE 3-PHOSPHATE
SIMILARITY).
ACTIVATES THIOL GROUP DURIN
(BY SIMILARITY).
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37A6CEA9376779E5 CRC64;
                                                                                                  ria; Firmicutes; Bacillales; Staphylococcus
TaxID=158878, 158879, 196620, 1280;
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SWISS-2DPAGE; Q9Z5C5; STAAN.

HSSP; P17721; 1HDG.

InterPro; IPR006424; GAPDH-I.

InterPro; IPR000173; GAP_dhdrogenase.

Pfam; PF02800; gpdh; 1.

Pfam; PF02800; gpdh C; 1.

PRINTS; PR00078; G3PDHDRGNASE.

TIGRFAMB; TIGR01534; GAPDH-I; 1.
(strain Mu50 / ... (strain MW2), a
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151 151 GLY
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EMBL; AP003360; BAB56934.1; -.
EMBL; AP003131; BAB41960.1; -.
EMBL; AP004824; BAB94599.1; -.
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                             aureus (aureus)
                                                                                                 Bacteria; Firmicutes;
NCBI_TaxID=158878, 158
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase C (EGAPC OR Z2304 OR ECS2022.
Escherichia coli 0157:H7.
                                                                                                                                                            GLYCERALDEHYDE
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                                     EMBL; AJ000339; CAA04014.1; -.
PIR; T09633; T09633.
HSSP; P17721; 1HDG.
InterPro; IPR000173; GAP_dhdrogenase.
InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; FALSE_NEG.
Glycolysis; NAD; Oxidoreductase.
BINDING 156 156 GLYCERALDE
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Pred.
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G3P3 ECO57
P58072;
16-OCT-2001
16-OCT-2001
28-FEB-2003
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                                                     MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFD
                                                                KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEALEGTVEVKDGGFDVNGKFI
                                                                                                                                         KDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGQFVKVSAEREPANIDWATDGV
                                                                                                                                                                                                 CTGFYTDKDKAQAHIEA-GAKKVLISAPATGDLKTIVFNTNHQELDGSETVVSGA
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                               87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GAPDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=B107;
MEDLINE=98240227; PubMed=9579064;
Branny P., Delatorre F., Garel J.R.;
Branny P., Delatorre F., Garel J.R.;
"An operon encoding three glycolytic enzymes in Lactobacillus delbrueckii subsp. bulgaricus: glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate kinase and triosephosphate
                                                                                                                     -DLN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
1yde 3-phosphate
            Length
                                Indels
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Bacteria, Firmicutes, Lactobacillales, Lactobacillaceae
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Microbiology 144:905-914(1998).

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate

NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.

-!- PATHWAY: Second phase of glycolysis; first step.

-!- SUBUNIT: Homotetramer (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosp dehydrogenase family.
           ۲;
                        2;
60;
          Score 1132.5; DB Pred. No. 3.9e-62; 1; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
yde 3-phosphate dehydrogenase (EC
                                                                                                               *||| ||| :| :| :| VDGGFRVNGKEVKSFSEPDASKLPWK--
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                                44;
          ch 49.7%;
l Similarity 54.7%;
231; Conservative
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O32755;
16-OCT-2001 (Re]
16-OCT-2001 (Re]
28-FEB-2003 (Re]
Glyceraldehyde 3
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
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ACTIVATES THIOL GROUP DURING
(BY SIMILARITY).
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7;
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K MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Hayashi T., Takami H., Honda T., Sasakawa C., Ogasawara M., Tobe T., Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. B:11-22(2001).

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NADH.

-!- CATALYTIC ACTIVITY: D-glyceroyl phosphate + NADH.

-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
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                                                                                                                                                                                                                                                                                                                                          phosphate
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ACTIVATES THIOL GROUP DURING CATAL (BY SIMILARITY).
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7
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Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD; M
BINDING 150 150 GLYCE
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nilarity 47.5%;
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12;
MEDLINE=97251357; PubMed=9097039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itc Aiba H., Baba T., Fujita K., Hayashi K., Mori T., Kitagawa M., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Kasai H., Kashimoto K., Miki T., Motomura K., Mori H., Mori T., Motomura Y., Nashimoto H., Nishio Y., Oshima T., Sait Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map."; DNA Res. 3:363-377(1996).
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STRAIN=K12;
Hidalgo E., Limon A., Aguilar J.;
"A second Escherichia coli gene with similarity to gapA.";
Microbiologia 12:99-106(1996).
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Hidalgo E., Chen Y.-M., Lin E.C.C., Aguilar J.;
"Molecular cloning and DNA sequencing of the Escherichia
ald gene encoding aldehyde dehydrogenase.";
                                                                                                                                                                                                                                                        STANDARD; PRT; 333 AA.
P33898; P76094; P78062; P78291; Q03850; Q63208;
01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase C (EC 1 Escherichia coli.
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STRAIN=River isolate, and Clinical is
MEDLINE=98283700; PubMed=9622357;
Espinosa-Urgel M., Kolter R.;
"Escherichia coli genes expressed preenvironment.";
Mol. Microbiol. 28:325-332(1998).
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Krawetz S.A., Connor W., Cannon P.D., Dixon G.H.;

Krawetz S.A., Connor W., Cannon P.D., Dixon G.H.;

Krawetz S.A., Connor W., Cannon P.D., Dixon G.H.;

Krawetz S.A., Connor W., Cannon P.D., Dixon G.H.;

Thibraries: evidence for a rat glyceraldehyde-3-phosphate

Thibraries: evidence for a rat glyceraldehyde-3-phosphate

Thibraries: evidence for a rat glyceraldehyde 3-phosphate

Thibraries: evidence for a rat glyceraldehyde 3-phosphate + DNA 5:427-435(1986).

L. CATALVIIC ACTIVITY: D-glyceraldehyde 3-phosphate + DATHWAY: Second phase of glycolysis; first step.

C. !- PATHWAY: Second phase of glycolysis; first step.

C. !- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

C. !- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

C. !- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.

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E88223297376B0A0
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STRAIN=K12;
MEDLINE=88232416; PubMed=2836696;
Nakamura H., Murakami H., Yamato I., Anraku Y.;
Nakamura Esquence of the cybB gene encoding "Nucleotide sequence of the cybB gene encoding "Nucleotide coli K12.";
Escherichia coli K12.";
Wal. Genet. 212:1-5(1988).
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Submitted (OCT-1990) to the EMBL/GenBank/DDBJ
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EMBL; AE000239; AAC74498.1; ALT FRAME.
EMBL; AE000239; AAC74499.1; ALT FRAME.
EMBL; D90780; BAA15033.1; ALT FRAME.
EMBL; D90781; BAA15038.1; ALT FRAME.
EMBL; N07841; -; N0T ANNOTATED CDS.
EMBL; X07569; -; NOT ANNOTATED CDS.
EMBL; X1721; 1HDG.
ECOGene; EG12103; GapC.
InterPro; IPR000173; GAP dhdrogenase.
InterPro; IPR000173; GAPDH-I.
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)
GAPA OR GAP OR MPN430 OR MP411.
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HSSP; P17721; 1HDG.
InterPro; IPR000173; GAP_dhdrogenase.
InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh_C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
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ton G., Kelley J
ky M., Fuhrmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATAL
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrman Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merric Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; Science 270:397-403(1995).
                                                                                                                                                               89;
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                                                                                                                                                                                                       337
TIGREAMB; TIGR01534; GAPDH-1; ...
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD; Complete proteome.
BINDING 157 GLYCERALDEHYDE 3-PHOSPHATE
(BY SIMILARITY).
CATTOR 184 ACTIVATES THIOL GROUP DURING (BY SIMILARITY).
                                                                                                                                     Length
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                                                                                                                                   DB 1;
                                                                                                                                    Score 870.5; DB 1;
Pred. No. 3.5e-46;
; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-81 AND 279-337 FROM N.A. STRAIN=ATCC 33530 / G-37; MEDLINE=94075230; PubMed=8253680; Peterson S.N., Hu P.-C., Bott K.F., Hutchison "A survey of the Mycoplasma genitalium genome sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glyceraldehyde 3-phosphate
GAPA OR GAP OR MG301.
Mycoplasma genitalium.
                                                                                                                                      38.2%;
                                                                                                                                                  43.8%;
                                                                                                                                                                Conservative
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                                                                                                                                                     Similarity
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01-FEB-1996
28-FEB-2003
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P47543;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GLYCERALDEHYDE 3-PHOSPHATE
(BY SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYSIS
(BY SIMILARITY).
                                     + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 337;
Bacteriol. 175:7918-7930(1993).
CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phonomete + phonomete + phonomete + phonomete + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phonometer + phon
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42.8%; Pred. No. 3.2e-45;
cive 52; Mismatches 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMB; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD; C
BINDING 157 157
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EMBL; U02213; AAD12507.1; -.
EMBL; U02178; AAD12463.1; -.
PIR; C64233; C64233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000173; GAP_dhd
InterPro; IPR006424; GAPDH-I
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HSSP; P17721; 1HDG.
TIGR; MG301; -...
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Best Local
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                                                                                                                                                                                                                                                                                                                        3032.";
                                                                                                                                                                                    Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphate kinase, and triosephosphate isomerase.";
J. Bacteriol. 174:6076-6086(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 MVVKVGINGFGRIGRLAFRRI-QNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGQFVKVSAEREPANIDWATDGVEIVL
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PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD; Complete proteome.
Glycolysis; Oxidoreductase; NAD; Complete proteome.
Glycolysis; Oxidoreductase; NAD; Complete proteome.
GLYCERALDEHYDE 3-PHOSPHATE.
GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING CATALYSIS.
ACT SITE 180 ACTIVATES THIOL GROUP DURING CATALYSIS.
ACT SITE 180 ACTIVATES THIOL GROUP DURING CATALYSIS.
CONFLICT 25 26 SD -> NG (IN REF. 1).
ACT SITE 180 ACTIVATES THIOL GROUP DURING CATALYSIS.
CONFLICT 25 26 SD -> NG (IN REF. 1).
                                                                                                                                                                                                                                                                                                                   "Complete genomic sequence of Corynebacterium glutamicum ATCC 1: Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

-! - CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate

NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.

-! - PATHWAY: Second phase of glycolysis; first step.

-! - SUBUNIT: Homotetramer.

-! - SUBCELLULAR LOCATION: Cytoplasmic.

-! - SUBCELLULAR LOCATION: Cytoplasmic.

-! - SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
                                                                            Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
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                                                    1.2.1.12}
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                        Last sequence update)
Last annotation update)
                                                    dehydrogenase (EC
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
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HSSP; P00362; 1GD1.
InterPro; IPR000173; GAP_dhdrogenase.
InterPro; IPR006424; GAPDH-I.
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Pred.
                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ATCC 13059 / AS019;
MEDLINE=93015645; PubMed=1400158;
Eikmanns B.J.;
"Identification, sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDDDSITVGGKRIAVYAERDPK-
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PR00078; G3PDHDRGNASE.
s; TIGR01534; GAPDH-I;
             Created)
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                                                  Glyceraldehyde 3-phosphate
GAP OR CGL1588.
                                      Last
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Q01651;
01-APR-1993 (Rel. 25,
28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02800; gpdh;
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PRINTS;
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MEDILINE=98044033; PubMed=9504437;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Broullet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J. Daniel R.A.,

Denizot F., Devine K.M., Dusterhoft A., Bhrlich S.D., Emmerson P.T.,

Fritz C., Fujita M., Fujita Y., Fuma S., Galisti S., Grandi G.,

Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,

Guiseppi G., Guy B.J., Haga K., Haerr-Blanchard M., Klein C.,

Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

Kuitta K., Lapidus A., Lardinois S., Mauel C., Medigue C.,

Medina N., Mellado R.P., Mixuno M., Moestl D., Nakai S., Noback M.,

Noone D., O'Reilly M., Ogawa K., Ogiwarla A., Oudega B., Prescott A.M.,

Prescan E., Pujic P., Purnelle B., Roche B., Rose M., Sadaie Y.,

Raiger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y.,

Raiger M., Rivolta C., Rocha B., Serror P., Shin B.S.,

Setiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,

Seliguchi J., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
                                                                                                                                                                                                                 325
                                                                                                                                                                                                                                                                                                                                                                                              272
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                                                                                                                                                                                                                                                                                                                                   AAKAIGLVIPELNGKLDGAAQRVPVPTGSVTELVVTLDKNVSVDEINAAMKAASNDSFG-
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                                                                                                                         EATSFFAKKEAAEKHLHANGAKKVVITAPGGNDVKTVVFNTNHDILD-GTETVISGASCT
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MEDLINE=89160255; PubMed=2493629;
Viaene A., Dhaese P.;
"Sequence of the glyceraldehyde-3-phosphate dehydrogenase gene
Bacillus subtilis.";
Nucleic Acids Res. 17:1251-1251(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase 1 (EC 1.2.
dependent glyceraldehyde-3-phosphate dehydrogenase)
GAPA OR GAP OR BSU33940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
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STRAIN=168;
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P09124;
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collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aymerich S.;
"Two glyceraldehyde-3-phosphate dehydrogenases with opposite physiological roles in a nonphotosynthetic bacterium.";
J. Biol. Chem. 275:14031-14037(2000).

-!- FUNCTION: More active in catabolism.

-!- FUNCTION: More active in catabolism.

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphane | NADH. |

-!- PATHWAY: Second phase of glycolysis; first step.

-!- SUBUNIT: Homotetramer.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     opposite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E., Branlant
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TIGRFAMs; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD; Multigene family; Complete INIT_MET 0 0
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ACTIVATES THIOL GROUP DURING
                                                                                                                                                                                                                                                    STRAIN=168 / JH642;
MEDLINE=96345629; PubMed=8755892;
Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
"Cold shock stress-induced proteins in Bacillus subtilis.'
J. Bacteriol. 178:4611-4619(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
MEDLINE=20261518; PubMed=10799476;
Fillinger S., Boschi-Muller S., Azza S., Dervyn
Aymerich S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVATES THIOL GRO
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EMBL; Z99121; CAB15399.1; -.
PIR; S02754; DEBSG.
HSSP; P00362; 1GD1.
Subtilist; BG10827; gapA.
InterPro; IPR000173; GAP dhdrogenase.
InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
Pfam; PF02800; gpdh C; 1.
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178 A
35701 MW;
                                                                                                                                                              Nature 390:249-256(1997).
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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1 MKKITGIILLLLAVIILSAC......EMSYTAQLVRTLEYFAKIAK US-10-650-369-22 2278 score: Sequence: Title: Perfect

448

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

SPTREMBL_25:*

1: sp_archea:*

2: sp_bacteria:*

4: sp_human:*

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6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

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10: sp_rodent:*

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SUMMARIES

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ALIGNMENTS

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PEGUENCE FROM N.A.

Perez-Casal J.F., Bolton A., Song X.-M., Willson P., Potter A.A.;

Perez-Casal J.F., Bolton A., Song X.-M., Willson P., Potter A.A.;

A perez-Casal J.F., Bolton A., Song X.-M., Willson P., Potter A.A.;

Tugs of the surface proteins GapC and Mig of Streptococcus

dysgalactiae as protective antigens against mastitis in non-lactating

cows.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF375662; AAP31408.1; -..

GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. .; IEA.)

R GO; GO:0006096; P:glycolysis; IEA.

InterPro; IPR000173; GAP—dhdrogenase.

Pram; PF00044; gpdh; 1.

Pram; PF02800; gpdh C; 1.

Pram; PF02800; gpdh C; 1.

PRINTS; PR00074; GAPDH-I; 1.

TIGRFAMS; TIGRO1534; GAPDH-I; 1.

TIGRFAMS; TIGRO1534; GAPDH-I; 1.

TIGRFAMS; TIGRO1534; GAPDH-I; 1.
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                                                                                                                                                      Streptococcus dysgalactiae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
NCBI_TaxID=1334;
                OBSZE7;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde 3-P dehydrogenase.
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Pred. No. 2.3e-88;
0; Mismatches 1;
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Best Local Similarity 79.6%;
Matches 335; Conservative
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s a Glyceraldehyde
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                                     KDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGOFVKVSAEREPANIDWATDG
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Seifert K.N., Bleiweis A.S., McArthur W.P., Brady L.J.;
"The Group B Streptococcal Surface Antigen Delta is a Glyceral
3-Phosphate Dehydrogenase.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
DEHYDROGENASE FAMILY.

EMBL; AF338416; AAK14387.1; -.

HSSP; P00362; IGD1.

GO; GO:00064365; F:glyceraldehyde-3-phosphate dehydrogenase (p. GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR006424; GAPDH-I.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF00844; gpdh, 1.

Pfam; PF02800; gpdh, 2; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase.
Streptococcus agalactiae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Pred. No. 5e-83;
5; Mismatches
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Best Local Similarity 74.1%; Pre
Matches 312; Conservative 15;
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PS00071; GAPDH; 1.
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Mol. Microbiol. 45:1499-1513(2002).

EMBL; AL766853; CAD47470.1; -.

SagaList; gbs1811; -.

GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. GO; GO:0006096; P:glycolysis; IEA.

InterPro; IPR006424; GAPDH-I.

InterPro; IPR000173; GAP_dhdrogenase.

Pfam; PF02800; gpdh, 1.

Pfam; PF02800; gpdh C; 1.

Pfam; PF02800; gpdh C; 1.

TIGRFAMs; TIGR01534; GAPDH-I; 1.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase.
GBS1811.
Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Fra
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74.1%; Pred. No. 5e-83;
ive 15; Mismatches
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STRAIN=2603 V/R / Serotype V;
MEDLINE=2222988; PubMed=12200547;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterso Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterso Wessels M.R., Daugherty S. Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S. DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Pedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Milacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Mai Fraser C.M.;
MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRF
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase.
GAP OR SAG1768.
Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcus.
NCBI_TaxID=216466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence and comparative genomic emerging human pathogen, serotype V Streptococcus Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002) EMBL; AE014272; AAN00631.1; -. TIGR; SAG1768; -. GO; GO:0004365; F:glyceraldehyde-3-phosphate dehyd: InterPro; IPR006424; GAPDH-I. InterPro; IPR006173; GAP_dhdrogenase.
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PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I;
PROSITE; PS00071; GAPDH; 1.
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Pfam; PF02800; gpdh
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Fontaine M.C., Perez-Casal J., Song X.-M., Shelford J., Willson P.J.,
                                                  Gaps
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"Immunization of dairy cattle with recombinant GapC and chimeric antigens confers protection against heterologous challenge with Streptococcus uberis.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                               1 MVKKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRF
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EMBL; AF421900; AAM73771.1; -. GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

InterPro; IPR00644; GAPDH-I.

InterPro; IPR000173; GAP_dhdrogenase.

Pfam; PF00044; gpdh; 1.

Pfam; PF02800; gpdh C; 1.

Pfam; PF02800; gpdh C; 1.

RIGRFAMS; TIGR01534; GAPDH-I; 1.

Oxidoreductase.
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OBKVU6;

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01-OCT-2002 (TrEMBLrel. 22, Created)

01-OCT-2003 (TrEMBLrel. 22, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Glyceraldehyde-3-phosphate dehydrogenase.

Streptococcus uberis.

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                Indels
DB 16;
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Score 1564.5; Di
Pred. No. 5e-83;
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|| Similarity 74.1%; Productive 15;
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STRAIN=S735;
Brassard J., Gottschalk M., Quessy S.;
"Cloning and purification of Streptococcus suis serotype glyceraldehyde-3-phosphate dehydrogenase.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
Streptococcus suis.
Bacteria; Firmicutes; Lactobacillales; Streptococcus.
NCBI_TaxID=1307
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CRC64;
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EMBL; AY167026; AAN86058.1; -...

GO; GO:0004365; F:glyceraldehyde-3-phosphate dehy

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0006096; P:glycolysis; IEA.

InterPro; IPR006424; GAPDH-I.

InterPro; IPR000173; GAP_dhdrogenase.

Pfam; PF00044; gpdh; 1.

Pfam; PF002800; gpdh_C; 1.

Pfam; PF02800; gpdh_C; 1.

PTGRFAMs; TIGR01534; GAPDH-I; 1.
                     DB 2;
                  Score 1559.5; DB 2;
Pred. No. 9.7e-83;
5; Mismatches 10;
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|| Similarity 73.9%;
| 311; Conservative
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                                                                                                    88 KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEALEGTVEVKDGGFDVNGKFIKVSAE
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                                                                                                                                                                                                                                                                                 CLAPMAKALHDAFGIQKGLMTTIHAYTGDQMILDGPHRGGDLRRARAGAANIVPNSTGAA
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC BAA-334 / TIGR4;
MEDLINE=21357209; PubMed=11463916;
Tettelin H., Nelson K.E., Paulsen I.T., Haft D.H., Dodson R.J., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                                              1 MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPVMLAHLLKYDTTQGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC11733;
Bergmann S., Hammerschmidt S.;
"Identification of pneumococcal GAPDH as plasmin(ogen)-binding protein.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007490; AAK76079.1; -.
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O1-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12).
SP2012 OR GAPDH.
Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
NCBI_TaxID=1313;
              13;
  7.2e-82
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MEDLINE=21429245; PubMed=11544234;
Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett Hoskins J., Fiborn W.E. Jr., Fritz L., Fu D.-J., Fuller W., Gering DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Gering Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., Leblanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
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Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-CT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-CT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-CT-2003 (TrEMBLrel. 25, Last annotation update)
G1-CT-2003 (TrEMBLrel. 25, Last annotation update)
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PIR; F95235; F95235.

HSSP; P00354; 3GPD.

TIGR; SP2012; -.

GO; GO:0006096; F:glyceraldehyde-3-phosphate dehydrogenase

GO; GO:0006096; P:glycolysis; IEA.

InterPro; IPR006424; GAPDH-I.

InterPro; IPR000173; GAP_dhdrogenase.

Pfam; PF02800; gpdh, I.

Pfam; PF02800; gpdh, I.

Pfam; PF02800; gpdh, I.

TIGRFAMS; TIGR01534; GAPDH-I; I.

PROSITE; PS00071; GAPDH-I; I.

Oxidoreductase; Complete proteome.

SEQUENCE 335 AA; 35856 MW; DA483CEA423E747B CRC64;
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Pred. No. 2.5e-81;
12; Mismatches 13;
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les 310; Conservative 1
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Mochren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,

Noris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,

Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,

Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud

Glass J.I.;

"Genome of the bacterium Streptococcus pneumoniae strain R6.";

J. Bacteriol. 183:5709-5717(2001).

R EMBL, AE008547; AAL00628.1; -.

R PIR, G98099; G98099.

GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. GO; GO:0006096; P:glycolysis; IEA.

R InterPro; IPR000173; GAPDH-I.

R Pfam; PF02800; gpdh, 1.

Pfam; PF02800; gpdh, 1.

Pfam; PF02800; gpdh, 2.

R TIGRFAMS; TIGR01534; GAPDH-I; 1.

R PROSITE; PS00071; GAPDH-I; 1.

R PROSITE; PS00071; GAPDH-I; 1.

R PROSITE; PS00071; GAPDH-I; 1.

R PROSITE; PS00071; GAPDH-I; 1.
                                            Skatrud
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QBKHG1;

QBKHG1;

Q1-OCT-2002 (TrEMBLrel. 22, Created)

01-OCT-2003 (TrEMBLrel. 22, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Glyceraldehyde-3-phosphate dehydrogenase.

Streptococcus agalactiae, and

Streptococcus iniae.

Bacteria; Firmicutes; Lactobacillales; Streptococcacea

Streptococcus.

NCBI_TaxID=1311, 1346;
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Best Local Similarity 73.6%;
Matches 310; Conservative 12
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                                                                       chimer
                    and 9117
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                                                                 "Immunization of dairy cattle with recombinant GapC and chime antigens confers protection against heterologous challenge wis streptococcus uberis.";

Streptococcus uberis.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

-!-SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
DEHYDROGENASE FAMILY.

EMBL; AF421899; AAM73770.1; -.

EMBL; AF421809; AAM73773.1; -.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

InterPro; IPR006424; GAPDH-I.

InterPro; IPR006424; GAPDH-I.

Pfam; PF00044; gpdh; 1.

Pfam; PF002800; gpdh; 1.

Pfam; PF02800; gpdh 1.

Pfam; PF02801; gpdh - I; 1.
                                                                                                                                                                                                                dehydrogenase
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                    STRAIN=ATCC 27541,
                                     Shelford
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QBKVU5;
QBKVU5;
QBKVU5;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2003 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase.
Streptococcus parauberis.
Streptococcus parauberis.
Streptococcus parauberis.
Streptococcus.
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Best Local Similarity 72.7%;
Matches 306; Conservative
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SPECIES=S.agalactiae, and E
Fontaine M.C., Perez-Casal
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                              chimeric
J., Willson
             Potter A.A.;

Immunization of dairy cattle with recombinant GapC and chimericantion of dairy cattle with recombinant GapC and chimericantion of dairy cattle with reterologous challenge with antigens confers protection against heterologous challenge with Streptococcus uberis.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE

DEHYDROGENASE FAMILY.

RMBL; AF421901; AAM73772.1; -.

EMBL; AF421901; AAM73772.1; -.

EMBL; AF421901; AAM73772.1; -.

RGO; GO:0006491; F:oxidoreductase activity; IEA.

RGO; GO:0006096; P:glyceraldehyde-3-phosphate dehydrogenase (p. RGO; GO:000644; gAPDH-I.

R InterPro; IPR00044; gAPDH-I.

R Pfam; PF00044; gpdh; 1.

R Pfam; PF00078; GAPDH-I; 1.

R PRINTS; PR00078; GAPDH-I; 1.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Extracellular glyceraldehyde-3-phosphate dehydrogenase
1.2.1.12).
GAPC OR SMU.360.
Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                        311647C25489AC9E CRC64;
Shelford
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 73.4%; Pred. No. 4.6e-81;
Matches 309; Conservative 13; Mismatches 14;
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 Song X.-M.,
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 ų.,
                                                                                                                                                                                                                                                                                                                                       36037 MW;
   Perez-Casal
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SEQUENCE 336 AA;
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448
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01-OCT-2000
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                               302;
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Best Local S
Matches 302
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                                                                                                                                                      EMBL;
HSSP;
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Q9L5X6
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i J.J.;
dental
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                                                                                                                     F "Gencime";

Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

R EMBL; AE014883; AAN58118.1; -.

EMBL; AE014883; AAN58118.1; -.

R GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. GO:0006096; P:glycolysis; IEA.

R GO; GO:0006096; P:glycolysis; IEA.

R GO; GO:0006096; P:glycolysis; IEA.

R InterPro; IPR006173; GAPDH-I.

R InterPro; IPR006173; GAP_dhdrogenase.

R Fam; PF02800; gpdh; 1.

R Ffam; PF02800; gpdh; 1.

R FINTS; PR00078; G3PDHDRGNASE.

R TIGRFAMS; TIGR01534; GAPDH-I; 1.

R NOXIGOREDICESE; Complete Proteome.

CW Oxidoreductase; Complete Proteome.

CM Oxidoreductase; Complete Proteome.

CM Oxidoreductase; Complete Droteome.

CM Oxidoreductase; Complete Droteome.

CM Oxidoreductase; Complete Droteome.
                                        [1]
SEQUENCE FROM N.A.
STRAIN=UA159 / ATCC 700610 / Serotype C;
STRAIN=UA159 / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Ajdic D., McShan W.M., McLaughlin R.E., Kenton S., Jia H., Lin S.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,
Carson M.B., Primeaux C., Tian R., White J., Roe B.A., Ferretti
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A.,
                                                                                                                                                                                                                                                                                                         337;
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    Streptococcaceae;
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Last annotation update)
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Pred. No. 1.7e-80;
3; Mismatches 15;
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   Firmicutes; Lactobacillales;
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01-MAR-2002 (TrEMBLrel. 20, C
01-MAR-2002 (TrEMBLrel. 20, L
01-OCT-2003 (TrEMBLrel. 25, L
Glyceraldehyde-3-phosphate de
GAPDH.
                                                                                                                                                                                                                                                                                                         ch
l Similarity 71.8%;
303; Conservative
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     Bacteria; Firmico
Streptococcus.
NCBI_TaxID=1309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 DPIVSSDIVGVSYGSLFDATQTKVMEVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAIGLVIPELNGKLDGAAQRVPVPTGSVTELVVTLDKNVSVDEINAAMKAASNDSFGYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 DPIVSSDIVGMSYGSLFDATQTKVLDVDGKQLVKVVSWYDNEMSYTSQLVRTLEYFAKIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 KDPEQIDWATDGVEIVLEIDGTVEVKEGGFEVNGQFVKVSAEREPANIDWATDGVEIVLE
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                                                                                              SEQUENCE FROM N.A.
STRAIN=LMG18311;
van den Bogaard P.T.C., Kleerebezem M., Hols P., Crispie F.,
Van den Bogaard P.T.C., Kleerebezem M., Hols P., Crispie F.,
Kuipers O.P., de Vos W.M.;
"Modulation of Glycolysis by Lactose Availability in Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85;
                                                                                                                                                                                                                                                                                                             GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. GO:0006096; P:glycolysis; IEA.
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR006424; GAPDH-I.
InterPro; IPR006424; GAPDH-I.
Pfam; PF000044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 336;
                                                                                                                                                                                                 thermophilus.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                   Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52C1F25F3A7E0230 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1513.5; DB 2;
Pred. No. 4.5e-80;
8; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 AA
Streptococcus thermophilus.
Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36026 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.4%;
illarity 71.7%;
Conservative 18
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                                                                                                                                                                                                                                                           DEHYDROGENASE FAMILY.
, AF442551; AAL35377.1;
, P00354; 3GPD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase.
SEQUENCE 336 AA;
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                                         Streptococcus.
NCBI_TaxID=1308;
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390
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                                                                                                                                                                                                                                                                                                                    151.EQIDWATDGVEIVLEIDGTVEVKEGGFEVNGQFVKVSAEREPANIDWATDGVE.
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                                                                                                                                                                                                                                  320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus gordonii.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae
                                                                                                                                                                                                                     6FFCC18BB01E91F0 CRC64;
glyceraldehyde-3-phosphate dehydrogenase
                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                  Score 1459.5; DB 2;
Pred. No. 5.7e-77;
4; Mismatches 15;
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320
33968 MW;
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PSO0071; GAPDH;
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                                                                                                                                                       InterPro; IPR000173;
Pfam; PF00044; gpdh;
Pfam; PF02800; gpdh
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320
320 AA;
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                                                 SEQUENCE FROM N.A.
                                                                                                                                                                             PRINTS; PRO0078;
                            Streptococcus.
NCBI_TaxID=1302;
                                                                                                                                                                                                  Oxidoreductase
 Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9AJT7;
Q9AJT7;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                  291;
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Best Local
Matches 29
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96 GNFIKVSAERDPENIDWATDGVEIVLEALEGTVEVKDGGFDVNGKFIKVSAEKDPEQIDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 GFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEVKEGGFEVN
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                                                                                                                                                                                                                                                                                                                                                                                                                              dehydrogenase
                                                                                                                                                                                                                                            Amezaga M.R., Carter P.E., Cash P., McKenzie H.; "Sequence variation in mef(A) and gap genes in M-phenotype erythromycin resistant Streptococcus pneumoniae."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                            Streptococcaceae;
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4e-74;
13;
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HSSP; P00362; 1GD1.
GO; GO:0004365; F:glyceraldehyde-3-phosphate de
GO; GO:0016491; F:oxidoreductase activity; IEA
GO; GO:0016491; F:oxidoreductase activity; IEA
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR006424; GAPDH-I.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
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Pred. No. 4e-74
[2; Mismatches
Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
                                                                                    Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales;
Streptococcus.
NCBI_TaxID=1313;
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32930 MW;
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TIGREAMS; TIGR01534; GAPDH-1;
PROSITE; PS00071; GAPDH; 1.
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STRAIN=clinical isolate;
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284; Conser
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Q9AJT9;
01-JUN-2001
01-JUN-2001
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EAAEKHL-KGGAKKVVITAPGGNDVKTVVFNTNHDVLDGTETVISGASCTTNCLAPMAKA 154
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                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=clinical isolate;

Amezaga M.R., Carter P.E., Cash P., McKenzie H.;

Amezaga M.R., Carter P.E., Cash P., McKenzie H.;

Amezaga M.R., Carter P.E., Cash P., McKenzie H.;

Sequence variation in meff(A) and gap genes in M-phenotype

"Sequence variation in meff(B) and gap genes in M-phenotype

"Sequence variation in meff(A) and gap genes in M-phenotype

"Sequence variation in meff(A) and gap genes in M-phenotype

"Sequence variation in meff(A)

EMBL SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE

DEHYDROGENASE FAMILY.

EMBL; AJ292046; CAC27446.1; -.

EMBL; AJ292046; CAC27446.1; -.

EMBL; AJ292046; CAC27446.1; -.

EMBL; AJ292046; CAC27446.1; -.

RSSP; PO0362; 1GD1.

ROS; GO:0006036; F:glyceraldehyde-3-phosphate dehydrogenase (P. GO; GO:0006036; P:glycolysis; IEA.

InterPro; IPR006424; GAPDH-1:

R Pfam; PF02800; gpdh, C; 1.

Pfam; PF02800; gpdh, C; 1.

Pfam; PF02800; gpdh, C; 1.

R PROSITE; PS00071; GAPDH-1: 1.

R PROSITE; PS00071; GAPDH-1: 1.

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                                        Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae.
Streptococcus.
NCBI_TaxID=1313;
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Best Local Similarity 71.6%; Pred. No. 4.6e-74;
Matches 283; Conservative 13; Mismatches 13;
1.2
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 dehydrogenase
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  Glyceraldehyde-3-phosphate
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309 AA;
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